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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 14, 2002, 08:48:29; Search time 12.59 Seconds (without alignments) 321.731 Million cell updates/sec Run on:

US-09-828-000-3 Title: Perfect score: Sequence:

1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Word size :

0

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Issued\_patents\_AA:\*
1: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/pcay Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB

Result

No matches found

Search completed: January 14, 2002, 08:50:22 Job time: 113 sec

WARD DEED WARE WARE

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A Accession: PH1525
A; Molecule type: protein
A; Residues: 18-27 cDUP>
A; Residues: 18-27 cDUP>
A; Experimental source: LAK cell
B; Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A; Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c A; Reference number: A40346; MUID:92002034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R; Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A; Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence A; Reference number: A28812; MUID:88273610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 18-41 <LIE>
A; Residues: 18-41 <LIE>
A; Residues: 18-41 awas also found
B; Dupuis, M.; Schaerer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med: 177, 1-7, 1993
A; Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A; Reference number: PH1525; MUID:93115648
                                                  R. McCauliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin J. Clin. Invers. 65, 1379-1391, 1990
A.7title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/A. Reference number: A37047; MUID:90237213
A.Reference number: A37047; MUID:90237213
A.Reference number: A37047; MUID:90237213
A.Residues: 1-417 AMCC.
A.Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A.Note: the authors translated the codon GTA for residue 349 as Tyr
B.Rokeach, L.A.; Hasalated the codon GTA for residue 349 as Tyr
B.Rokeach, L.A.; Hasalated the authors translated the authors translated the authors translated the codon GTA for residue 349 as Tyr
A.Note: the authors translated the autoantigen calreticulin.
A.Title: Characterization of the autoantigen calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A40346
A; Molecule type: protein
A; Residues: 18-34, "R' <ROJ>
R; Krause, K. H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
B; Krause and J. 270, 545-548, 1990
A; Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-pu
A; Reference number: S11475; MUID: 90380058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S11475
A; Molecule type: protein
A; Residues: 18-32 < KRA>
A; Residues: 19-32 < KRA>
A; Residues: 19-32 < KRA>
A; Reference to the EMBL Data Library, November 1996
A; Description: Characterization by genomic sequence analysis of a gene-rich 111 kb
A; Reference number: 222906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-417 <ROK>
A;Cross-references: GB:M84739; NID:g179881; PIDN:AAA51916.1; PID:g179882
                               A;Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536) R;McCauliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:125179; OMIM:109091
A; Map position: 19p13.3-19p13.2
A; Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A; Note: CRTC
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C; Keywords: calcium binding; integrin binding
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-417/Product: calreticulin #status predicted <AMI>
F;414-417/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-417 < LAM>
A; Cross-references: EMBL, AD000092; PIDN: AAB51176.1
A; Experimental source: Cell line 5HL2-B; fibroblast C; Comment: Autoantibodies specific for this protein
A; Residues: 1-417 <MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T45075
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A46452
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Calreticulin precursor - human
N;Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
N;Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C;Accession: A42330; A37047; A446452; A28812; PH1525; A40346; S11475; T45075
R;McCauliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J Blol. Chem. 267, 2557-2562, 1992
J;Blol. Chem. 267, 2557-2562, 1992
A;Fitler: The 5'-flanking region of the human calreticulin gene shares homology with the A;Accession: A42330; MUID:92129342
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                                                                                                                                                                                                                                                                                                                                                     1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180
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GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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                                                                                                                                                                       January 14, 2002, 08:49:15
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    protein search, using sw model

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S43376
S36799
JH0795
S29130
S29129
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A32507
A56637
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S06763
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Maximum DB seq length: 2000000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
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                                                                                                              OM protein
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are found in Sjogren's syndrome a

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Calleding precursor. Tath

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A;Residues: 18-36 <VAN-
A;Residues: 18-36 vAntei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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S06763
Caltesticulin pracursor - mouse
NALeraticulin pracursor - mouse
S06763
Caltesticulin pracursor - mouse
NALeraticulin pracursor - mouse
Species: 10-80-1999 #sequence_revision 10-80-1999 #text_change 10-80-1999
C; paccies: 10-80-1999 #sequence_revision 10-80-1999 #text_change 10-80-1999
C; paccies: 10-80-1999 #sequence_revision 10-80-1999
C; paccies: 10-80-1999 #sequence_revision 10-80-1999
R; Smith, M.J.; Koch, G.L.E.
EMBO 3. 9. 353-3586, 1999 #sext_change 10-80-1999
A; Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a mathodox: S06763, MULD:90059955
A; Rosiduce: S06763, MULD:90059955
A; Rosiduce: 18-416 - KSM.
A; Rosiduce: 18-416 - KSM.
A; Rosiduce: 18-416 - KSM.
A; Rosiduce: 18-414 - KSM.
A; Rosiduce: 18-4144 - KSM.
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                                                                                                                                                                                                                                                                                              78 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 137
                                                                                                                                                                                                                                                                                                                                                                                   121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                      Length 417;
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C; Keywords: calcium binding
Fp:1-17, Domain: signal sequence #status predicted <SIG>
Fp:48-416/Product: calregulin #status experimental <MAT>
F; 413-416/Region: endoplasmic reticulum retention signal
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Mismatches 0;
                      DB 1;
               Score 180; DB 1;
Pred. No. 7e-184;
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100.0%; Pred. No. 5.2e-7
tive 0; Mismatches
                                                                            Mismatches
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               100.0%;
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                                                                            Conservative
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Matches 77; Conserv
                                            Similarity
                                                                            Matches 180:
               Query Match
Best Local S
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Dec-1993 #Sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C;Accession: S36799; S36800
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of_calreticuli A;Reference number: S36799; MUID:93385184
                                                                                                                                                                                                                                                                                                                                                            brain coding for two isoforms of calreticuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 LDQTDMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIV 159
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                                         T.; Isobe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;397-400/Region: endoplasmic_reticulum retention signal
F;120-146/Disulfide bonds: #status experimental
F;162/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Superfamily: calreticulin
C. Keywords: calcium binding; glycoprotein
C. Keywords: calcium binding; glycoprotein
F. 1-14/Domain: signal sequence #status predicted <81G>
F. 35-42/Product: calreticulin, brain isoform 2 #status predicted <1
F. 348-42/Product: calreticulin, brain isoform 2 #status predicted <1
F. 341-16/7/Disulfide bonds: #status predicted
F. 341-16/7/Disulfide bonds: #status predicted
F. 383/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 400;
                                      R;Matsuoka, K.; Setä, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, Biochem. J. 298, 435-442, 1994
A;Title: Covalent structure of bovine brain calreticulin.
A;Reference number: S43376; MUID:94183174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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llarity 100.0%; Pred. No. 5.2e-58;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calreticulin precursor, brain isoform 2 - bovine
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: calcium binding; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                      RiLiu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine
                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S36799; MUID:93385184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 45-63,'E',65-83 <LIU>
A; Experimental source: brain, clone 8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: brain, clone 9.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 100.0
Matches 62; Conservative
                                                                                                                                                                                                                                                            A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: calreticulin
            C; Accession: S43376; S36801
                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-400 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 62; Conserv
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A; Residues: 1-421 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 35-45 <LI2>
                                                                                                                                                                   A; Accession: S43376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S36799
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Best Local S
Matches 62
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A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage A;Reference number: $13045; MUD:91054414
A;Reference number: $13045; MUD:91054414
A;Accession: $13045
A;Accession: $13045
A;Molecule type: protein
A;Residues: 18-29 <TRE>
C;Superfamily: calreticulin
C;Superfamily: calreticulin
E;1-17/Domain: signal sequence #status predicted <SIG>
F;18-416/Product: calreticulin #status experimental <MAT>
F;204-212/Region: nuclear location signal
F;413-416/Region: endoplasmic reticulum retention signal
F;344/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Bjochen. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A24154
A24154
A24154
A24154
Calreticulin precursor, skeletal muscle - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34154; S13047
B;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M. J. Stilegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M. J. Stiles Molecular cloning of the high affinity calcium-binding protein (calreticulin) A;Feference number: A34154; MuID:90094320
A;Accession: A34154
A;Status: preliminary
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S43376
calreticulin, brain isoform 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDN 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                42.8%; Score 77; DB 2; Length 416; 100.0%; Pred. No. 5.2e-74;
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F;1-17/Domain: signal sequence #status predicted <SIG>
F;415-418/Region: endoplasmic reticulum retention signal
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100.0%; Pred. No. 5.2e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. nc.
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Best Local Similarity 100.0
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Matches 77; Conservative
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A;Residues: 19-32 <TRE>
C;Superfamily: calreticulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-418 <FLI>
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R;Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A;Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran A;Reference number: S71342; MUID:96234004
A;Accession: S71343
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S29129
R;Treves, S.; Zorzato, F.; Pozzan, T.
Blochem. J. 287, 579-581, 1992
A;Title: Identification of calreticulin isoforms in the central nervous system. A;Reference number: S29129; MUID:93074997
A;Recession: S29129
A;Rocession: S29129
A;Roc
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A; Molecule type: mRNA
A; Residues: 1-419 < YAM>
A; Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAA11425.1; PID:g1514957
C; Superfamily: calreticulin
C; Keywords: calcium binding; endoplasmic reticulum
C; Keywords: calcium binding; endoplasmic reticulum
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-419/Product: calreticulin #status predicted <MAT>
F;205-213/Region: unclear location signal
F;415-418/Region: endoplasmic reticulum retention signal
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C;Species: Rana rugosa (Korean frog)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C;Accession: S71343
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                                   F;381-384/Region: endoplasmic reticulum retention signal F;316/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                       Length 384
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                       12.2%; Score 22; DB 2; Le
100.0%; Pred. No. 2.2e-15;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                151 FTHLYTLIVRPDNTYEVKIDNS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 FTHLYTLIVRPDNTYEVKIDNS 172
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                                                                                                                                                                                                       Query Match 12.2
Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                      N;Alternate names: protein 407
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Accesion: 140795; B31409; F60977
R;Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A;Title: Long-term sensitization training in aplysia leads to an increase in calreticulia A;Accession: J40795; MUID:93098937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecula typo: mRNA
A; Realdues: 1-405 < KENN
A; Realdues: 1-405 < KENN
A; Cross-references: GB:551239; NID:9262053; PIDN:AAB24569.1; PID:9262054
A; Kxperimental source: abdominal ganglion and antral nervous system
A; Kxperimental source: abdominal ganglion and antral nervous system
B; Kennody, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A; Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: protein

A; Molecule type: protein

R; Realduce: /x', 17-28, 'x', 20-31 < KE2>

R; Realduce: /x', 17-28, 'x', 20-31 < KE2>

R; Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.

Electrophoresis 10, 152-157, 1989

Electrophoresis 10, 152-157, 1989

A; Title: Development of a database of amino acid sequences for proteins identified and in A; Reference number: A60977; MUID:89276264

A; Accession: F60977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
s29130
calreticulin (clone 8) - African clawed frog (fragment)
c.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Species: 190-56p-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C.Accession: 329130; 701068
R.Trivos, S.; Zorzato, F.; Pozzan, T.
Biochem J. 287, 579-581, 1992
A;Title: Identification of calreticulin isoforms in the central nervous system.
A;Accession: $29130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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A)Accession: T01068
A)Stitus: translated from GB/EMBL/DDBJ
A)Molecule type: mRNA
A)Residues: 1-339, XTGR' <TRW>
A)Residues: 1-339, XTGR' <TRW>
A)Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 27; DB 1; Le
ilarity 100.0%; Pred. No. 1.1e-20;
Consorvative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           calreticulin precursor - California sea hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A94207; MUID:88320566
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Regidues: 'X',17-28,'X',30-31 <SWE>
Superfamily: calreticulin
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C; Superfamily: calreticulin
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Matches 27; Conserve
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A; Residues: 1-384 <TRE>
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Query Match

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Search completed: January 14, 2002, 08:51:14 Job time: 119 sec
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A; Residues: 1-406 cSMX>
A; Reference extracted from NCBI backbone (NCBIN:128274, NCBIP:128275)
B; McCauliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
A; Title: A human Ro/SS-A autoantique is the homologue of calreticulin and is highly home A; Reference number: A37158; MUID:90307981
A; Recession: A37158
A; Recession: A37158
A; Recellminary; nucleic acid sequence not shown; not compared with conceptual tra
A; Residues: 91-105, A*, 107, 109-124; 182-183, 'L', 185-220 cMCC>
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A56637

Calreticulin homolog precursor - fruit fly (Drosophila melanogaster)

N'Alternate names: Ro/SS-A autoantigen/calreticulin homolog

C.Species: Drosophila melanogaster

C; Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999

R; Accession: A56637; A37158

R; Smith, M.J.

DNA Seq. 3, 247-250, 1992

A; Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin |

A; Reference number: A56637; MUID:93208374
                                                                                                                                                                           Title: Isolation antigen - nematode (Onchocerca volvulus) (fragment)
C; Species: Onchocerca volvulus
C; Species: A32507; A28813
A; Title: Invest: 82, 262-269, 1988
A; Title: Isolation and characterization of expression cDNA clones encoding antigens of (A; Reference number: A92769; MuID:88273584
A; Reference number: A92769; MuID:88273584
A; Residues: I-336 vcNN>
C; Superfamily: calreticulin
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C; Keywords: calcium binding; endoplasmic reticulum
E:1-17/Domain: signal sequence #status predicted <SIG>
F; 403-406/Region: endoplasmic reticulum retention signal
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100.0%; Pred. No. 3.2e-12;
tive 0; Mismatches 0;
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A;Cross-references: FlyBase:FBgn0005585
171 HLYTLIVRPDNTYEVKIDNS 190
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Matches 19; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model protein January 14, 2002, 08:49:34; Search time 11.77 Seconds Run on:

(without alignments)
560.720 Million cell updates/sec

US-09-828-000-3

score: Perfect sc Sequence:

EPAVYFKEQFLDGDGWTSRW.......PDNTYEVKIDNSQVESGSLE 180

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

18 Word size :

σ Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Listing first 45

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P27797 homo sapien	P14211 mus musculu	P18418 rattus norv	P15253 oryctolagus	P52193 bos taurus	P42918 bos taurus	P28491 sus scrofa	P11012 onchocerca	P29413 drosophila
SUMMAKIES	ID	CRTC_HUMAN	CRTC_MOUSE	CRTC_RAT	CRTC_RABIT	CRT1_BOVIN	CRT2_BOVIN	CRTC_PIG	RAL1_ONCVO	CRTC_DROME
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## ALIGNMENTS

	(ERP60) (	Euteleosto Homo,	, Unnasch
PRT; 417 AA.	01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 02-AUG-2001 (Rel. 40, Last annotation update) CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (E	RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A). CALR OR CRTC. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalla: Eutheria; Primates; Catarrhini; Hominidae: Homo.	NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-22013129; PubMed-1919005; MCKeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch Greene B.M., Hoch S.O.;
STANDARD; P.	01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 01-AUG-2001 (Rel. 40, Last annotation update) CALRETICULIN PRECURSOR (CRP55) (CALREGULIN)	RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A). CALR OR CRTC. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Mammalia: Eutheria; Primetes; Catarhin	NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-92013129; PubMed=1919005; ROKeach L.A., Haselby J.A., Meilo Greene B.M., Hoch S.O.;
CCTC_HUMAN ID CRTC_HUMAN AC P27797;	01-AUG-1992 01-AUG-1992 20-AUG-2001 CALRETICULIN	RIBONUCLEOPROTEIN AUT CALK OR CRTC. Homo sapiens (Human). Eukaryota, Metazoa; ( Mammalia: Eutheria:	NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-92013129; Pubmen Rokeach L.A., Haselby J Greene B.M., Hoch S.O.;
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TISSUE—Colon carcinoma;
MEDLINE=97295306; PubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
J. H., Cancellor and Carabase of human colon carcinoma proteins.";
Electrophoresis 18:605-613(1997).
I. FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFIRITY CALCIUM-BINDING SITES.
I. SUBDUIT: MONOMER (BY SIMILARITY.
I. SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
I. SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
I. SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
I. CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
                                                              SEQUENCE FROM N.A. MEDILHE-90237213; PubMed-2332496; MEDILHE-90237213; PubMed-2332496; MCGauliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., NewKirk M.M., Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-92129342; PubMed-1733953; MCCauliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.; "The 5'-flanking region of the human calreticulin gene shares homology with the human GRP78, GRP94, and protein disulfide isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
"In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calreficulin) with a highly conserved amino acid sequence in the cytoplasmic domain of integrin alpha subunits.";
Bjochemistry 30:9859-9866(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trause H., Simmerman H.K.B., Jones L.R., Campbell K.P.; "Sequence similarity of calreticulin with a Ca2(+)-binding protein that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
                                                                                                                                                                      Molecular cloning, expression, and chromosome 19 localization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gel
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"Microsequences of 145 proteins recorded in the two-dimensional
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamerdin J., McCready P., Stilwagen S., Ramirez M., Carrano A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=3315,045; PubMed=1286669;
Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier |
Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier |
Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas
Appel R.D., Hughes G.J.;
"Human liver protein map a reference database established by
microsequencing and gel comparison.";
Electrophoresis 13:992-1001(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
"Characterization of the autoantigen calreticulin."; J. Immunol. 147:3031-3039(1991).
                                                                                                                                                                                               human Ro/SS-A autoantigen.";
J. Clin. Invest. 85:1379-1391(1990).
                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 267:2557-2562(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
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            the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPAVYFKEQFLDGDGWISRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 180; DB 1; Length 417; ilarity 100.0%; Pred. No. 5e-178; Conservative 0; Mismatches 0; Indels
 the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY,
PREVENT SECRETION FROM ER.
MISSING (IN REF. 3).
BC37C3C0F1054FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Andoplusmic reticulum; Calcium-binding; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 X APPROXIMATE REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                CALRETICULIN
                                                                                                                                                                                                                                                                                                             PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
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PRINTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
                                                                                                                                                                                                                                           InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_target.
                                                                                                                                               PIR; S11475; S11475.
PIR; A42330; A42330.
PIR; A46452; A46452.
SWISS-2DPAGE; P27797; HUMAN.
Aurhus/Ghont-2DPAGE; 9401; IEF.
HSC-2DPAGE; P27797; HUMAN.
                                                                                                                     EMBL; AD000092; AAB51176.1; -. PIR; A37047; A37047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48141 MW;
                                                                                            EMBL; M84739; AAA51916.1; -.
                                                                                                            EMBL; M32294; AAA36582.1;
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417 AA;
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Matches 180; Conserv
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CRTC_MOUSE
ID CRTC_MO
AC P14211
AC P14211
DT 01-JAN
DT 15-DEC
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(Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 37, Last annotation update)

01-JAN-1990 01-JAN-1990 15-DEC-1998

PRT;

STANDARD;

CRTC\_MOUSE P14211;

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                                                                                                                                                                                                                                                                                                                                            MEDINE-93013037; PubMed-1398135; Mazzarella R.A., Gold P., Cunningham M., Green M.; Green M.; Fall R.A., Gold P., Cunningham M., Green M.; Fall R.A., Gold P., Cunningham M., Green M.; Estermination of the sequence of an expressible cDNA clone encoding Espeó/calregulin by the use of a novel nested set method."; Gene 120:217-225(1992).
                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
STRAIN=BALB/C; TISSUE-Liver;
MEDLINE-90059955; PubMed=2583110;
Smith M.J., Koch G.L.E.;
Fulliple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
EMBO J. 8:3581-3586(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
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EMBL; M92988; AAA37569.1; --
PIR; S06763; S06763.
PIR; JC1444; JC1444.
SWISS-2DPAGE; P14211; MOUSE.
MGD; MG188252; CALT.
InterPro; IPR001580; CAlreticulin.
InterPro; IPR001580; CAlreticulin.
Probom; PR00626; CALRETICULIN.; PROSTE; PR00046; CALRETICULIN.
PROSTE; PS00004; CALRETICULIN.; PROSTE; PS000056; CALRETICULIN.; PROSTE; PS000055; CALRETICULIN.; PS0
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9-2-13
                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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308
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                                            Mus musculus (Mouse)
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REPEAT
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                                                                                                     104 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDN 163
                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K., Okinaga S., Kobayashi T.;
"An endoplasmic reticulum protein, calreticulin, is transported into Exp. Cell Res. 205:101-110(1993).
                                                                                    Gaps
                                                                                                                                                                                                                    CRTC_RAT STANDARD; PRT; 416 AA.
P18418; P10452;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (CALBP)
(CALCIUM-BINDING PROTEIN 3) (CABP3).
                                                                                                                                                                                                                                                                                                                                                                                                   Holmes C., Patel Y.C.; "Structural homology between the rat calreticulin gene product and the Onchocerca volvulus antigen Ral-1."; Nucleic Acids Res. 18:4933-4933(1990).
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Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
Maclennan D.H., Meldolesi J., Pozzan T.;
"Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
Blochem. J. 271:473-480(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson D.G., Mieskes G.; "Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the endoplasmic reticulum.";
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                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain cortex;
MEDLINE-90370496; PubMed-2395661;
Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE DAWLEY, TISSUE-Liver;
MEDLINE-95181573; PubMed-7876339;
Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
                                                              Length 416;
                                                             42.8%; Score 77; DB 1; Length 416
100.0%; Pred. No. 9e-72;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lone Y.C., Bailly A., Latruffe N.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
ASP/GLU/LYS-RICH.
BY SIMILARITY.
PREVENT SECRETION FROM ER.
24C03B00913408D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY;
MEDLINE-93202172; PubMed-8453984;

    Cell Sci. 107:2705-2717(1994).

407 AS
163 BY
416 PF
47994 MW;
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                                                                                                                                              164 TYEVKIDNSQVESGSLE 180
                                                                                                                                                          181 TYEVKIDNSQVESGSLE 197
                                                   Query Match
Best Local Similarity 100...
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of protein disulfide isomerase and calreticulin as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune antigens in LEC strain of rats.";
Biochim. Biophys. Acta 1158:339-344(1993).
LOW LINGTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
-: SUBUNIT: MONOMER (BY SIMILARITY).
-: SUBGLIULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-: SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-: CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE D-BETA-HYDROXYBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94072621; Pubmed-8251535;
Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
                                                                                                                                                                         rat
STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
BDELINE-92560010; PubMed-1497655;
Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
"Calreticulin is present in the acrosome of spermatids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLU/LYS-RICH.
BY SIMILARITY.
PREVENT SECRETION FROM ER.
2E6713CED31A2970 CRC64;
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PROSITE; PS00803; CALRETICULIN_1: 1.
PROSITE; PS00804; CALRETICULIN_2: 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
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EMBL; X79327; CAA55890.1; -.
PIR; S12085; S10205.
PIR; S13045; S13045.
PIR; A49176; A49176.
PIR; S45036; S45036.
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InterPro; IPR000886; ER_target.
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416 AA;
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CRTL_BOVIN
ID CRTL_BOVIN
AC P52193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guan S., Falick A.M., Williams D.E., Cashman J.R.;

"Evidence for complex formation between rabbit lung flavin-containing monocygenase and calreatculin.";

#INCOMPAGE THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW APPINITY CALCIUM-BINDING SITES.

-1 SUBBUIT: MONOMER (BY SIMILARITY).

-1 SUBBUIT: BELONG TO THE CALREITCULUM LUMEN.

-1 SIMILARITY: BELONGS TO THE CALREITCULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Slow-twitch skeletal muscle;
MEDLINE-90094320; PubMed-2600080;
Filegel L., Burns K., Maclennan D.H., Reithmeier R.A.F., Michalak M.;
Molecular cloning of the high affinity calcium-binding protein
(calreticulin) of skeletal muscle sarcoplasmic reticulum.";
J. Biol. Chem. 264:21522-21528(1989).
                                                                                                  104 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDN 163
                                                                                                                         121 DMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDN 180
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
             Score 77; DB 1; Length 416;
Pred. No. 9e-72;
0; Mismatches 0; Indels
42.8%; Scor. 100.0%; Pred. No. 3. 0. Mismatches 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fust-twitch skeletal muscle; MEDLINE-91282795; PubMed-2059224;
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MEDLINE-92002038; PubMed-1911780;
                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                     164 TYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                181 TYEVKIDNSOVESGSLE 197
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                        Bost Local Sim:
Matches 77;
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P15253;
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                 Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryota, Metazooa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bovinae, Bos
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 1; Length 418;
Pred. No. 9e-72;
0; Mismatches 0; Indels
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PREVENT SECRETION FROM ER.
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B6082B689DC763A6 CRC64;
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ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALRETICULIN
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PIR; F33208; F33208.

PIR; S13046; S13046.

PIR; S13047; S13047.

InterPro; IPR001580; Calreticulin.
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Pfam; PF00262; calreticulin; 1.
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PIR; C33208; C33208.
PIR; D33208; D33208.
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198
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Sus scrofa (Pig).
           calreticulin.
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REPEAT
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                           Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.; "Covalent structure of bovine brain calreticulin."; Biochem. J. 298:435-442(1994).
                                                                                                                                                                                                                                                                                                                                            REVENT SECRETION FROM ER (POTENTIAL). 7D4B68DFC689EEF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                    -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                           PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
Endoplasmic reticulum; Calcium_binding; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                  Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                             -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-i- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
InterPro; IPRO01580; Calreticulin.
InterPro ENCO262; Calreticulin; 1.
PRINTS; PRO0626; CALRETICULIN; 1.
                                                                                                                                                                                                                                    4 X APPROXIMATE REPEATS.
1-1.
1-2.
                                                                                                                                                                                                                                                                                 X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 1; L
Pred. No. 2.6e-56;
0; Mismatches 0;
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                                                                                                                                                                                                         N-DOMAIN
                                                                                                                                                                                                                           C-DOMAIN
                                                                                                                                                                                                                                                                                                                                              PREVENT
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                                                                                                                                                   ProDom; PD001866; Calreticulin; 1. PROSITE; PS00014; ER_TARGET; 1.
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MEDLINE-93385184; PubMed-8373827;
                          TISSUE-Brain;
MEDLINE-94183174; PubMed-8135753;
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                                                                                                                                                                                                                                                                                                                                                                                 34.4%; Somilarity 100.0%; Processive 0;
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291
400
238
185
204
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                                                                                      -!- SUBUNIT: MONOMER
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Matches 62; Conserv
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NCBI_TaxID=9913;
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P42918;
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RP 161
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                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                          Biochim. Biophys. Acta 1202:70-76(1993).
-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
-!- SUBGNIT: MONOMER (EN SIMILARITY).
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
"Comparison of cDNAs from bovine brain coding for two isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL). PREVENT SECRETION FROM ER. 0257E959F71528BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ς.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.4%; Score 62; DB 1; Length 421; 100.0%; Pred. No. 2.7e-56; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALRETICULIN, BRAIN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS0001466; Calreticulin; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULN_1; 1.
PROSITE; PS00805; CALRETICULN_2; 1.
PROSITE; PS00805; CALRETICULN_REPEAT; 3.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
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4 x APPROXIMATE REPEATS.
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P-DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L13462; AAC37307.1; -.
InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_target.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
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Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                         MEDLINE-88273584; PubMed-2455736;
Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
"Isolation and characterization of expression cDNA clones encoding
antigens of Onchocerca volvulus infective larvae.";
J. Clin. Invest. 82:262-269(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophillae; Drosophila.
                            MEDLINE-94341871; PubMed-7520419;
Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
"Epitopes of the Onchocerca volvulus RALI antigen, a member of the
calreticulin family of proteins, recognized by sera from patients
with Onchocerciasis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 388;
Pred. No. 5.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
9537F298A2D31CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAL-1 PROTEIN.
4 X APPROXIMATE REPEATS.
1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 X APPROXIMATE REPEATS. 2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRTC_DROME STANDARD; PRT; 406 AA.
P29413; Q9VHA3;
01-APR-1993 (Rel. 25, Created)
1-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
calreticulin Precursor (CRP55) (Calreculin) (HaCBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG/LYS-RICH (BASIC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; Prouzoz; carrectionin.
PRINTS; PRO0626; CALRETICULIN.
PRODOM; PD0010666; CALRETICULIN.1.
PROSITE; PS00803; CALRETICULIN.1; 1.
PROSITE; PS00804; CALRETICULIN.2; 1.
PROSITE; PS00805; CALRETICULIN.REPEAT; 3.
CALCIUM-binding; Repeat; Antigen; Signal.
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M20565; AAA59056.1; -.
PIR; A3267; A32507.
Interpro; IPR001580; Calreticulin.
Pfam; PF00262; calreticulin; 1.
                                                                                                                                  Infect. Immun. 62:3696-3704(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 IMFGPDICGPGTKKVHVIF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 IMFGPDICGPGTKKVHVIF 131
                                                                                                                                                                             SEQUENCE OF 53-388 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 19; Conserva
                                                                                                                    onchocerciasis
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189
2208
225
242
257
257
271
285
353
388 AA;
[1]
SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                       TISSUE-Uterus;
WEDLINES-91201375; PubMad-2016321;
WEDLINES-91201375; PubMad-2016321;
Wilner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
Vance J.E., Opas M., Michalak M.;
Vance J.E., Sancothmuscle sarcoplasmic reticulum and liver endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                               TISSUE-Small intestine;
MKDLINE-96327607; PubMed-8672129;
Winteroo A.K., Fredholm M., Davies W.;
"Evaluation and Characterization of a porcine small intestine CDNA 11brary: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioldea;
Onchoceroldae; Onchocerca.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 266:7155-7165(1991).
-:- FUNCTION: THIS PROTEIN BINDS CALCIUM, THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
-:- SUBGNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-:- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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105 AA; 11958 MW; D203B53FE36BDE1E CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001580; Calreticulin,
Pfam; PF00046; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN; 1.
PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
PROSITE; PS00805; CALRETICULIN_REPRAT; PARTIAL.
Endoplasmic reticulum; Calcium-binding; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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nes 25; Conserv
                                                                                                                                                                                                                                      SEQUENCE OF 18-32.
                                                                               SEQUENCE FROM N.A.
                                    WCBI_TaxID-9823;
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P11012;
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SEQUENCE
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EMBL; AE003683; AAF54416.1;

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RAMANA CEOTOGEN, C. CEDINGER,
RAMANATION, C., ROGETS Y.-H.C., Blazel, R., Champe M., Pfeiffer B.D.,
RAMANATHON, C., ROGETS Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
RAMAN K.H., DOYLE C., BAXTER E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RAMADII J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Bladaley E.M.,
Ballew R.M., Bancos P.V., Berman B.P., Bhandari D., Bladalakov S.,
RAMADII J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Bladaley E.M.,
Ballew R.M., Bachos P.V., Berman B.P., Bhandari D., Bladalakov S.,
RAMADIN S.J., Bouch J., Buluk C., Davenport L.B., Dovitter P.,
RAMELIS K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RAMADIN S.J., Evangelista C. C., Perraz C., Perriera S., Fleischman W.,
RAMADIN S.J., Evangelista C.C., Ferraz C., Ferraz C., Perriera S., Plasser K.,
ROGET C., Gabriellan A.E., Garp N.S., Gelbart W.M., Classer K.,
ROGET C., Gabriellan A.E., Garp N.S., Gelbart W.M., Classer R.,
ROGOR F., Gorbiellan A.E., Gary N.S., Gelbart W.M., Classer R.,
RAMEL B., Kalush F., Karpen G.H., Ke Z., Kenlson J.A., Ketchum K.A.,
RAMEL B., Kodira C.D., Kraft C., Mortis J., Mosherson D.L.
RAMEL B. McIntosh T.C., Morted W.P., Morton R.,
Ramadia M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,
Rabon D.R., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,
Rabon D.R., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,
Rabon D.R., Woy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.K.,
Rabon D.R., Woy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.K.,
Rabon D.R., Woy M., Murphy B., Murphy L., Walssehabeth J.,
Rabon D.R., Woodeger C., Turner R., Venter E., Wang A., Y., Wassarman D.A., Weillams S.M., Woodeger T., Warsarman D.A., Weillams S.M., Woodeger T., Smith H.,
Rabeng X.H., Zhong P.L., Zhong W., Zhon R., Shue B.C., Shen H.,

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McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin homologue."; DNA Seq. 3:247-250(1992).
                                                                       SEQUENCE FROM N.A.
MEDLINE-93208374; PubMed-1296819;
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BERKELEY;
NCBI_TaxID-7227;
                                                                                                                                                           Smith M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra J.D.;
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EMBL; X64461; CAA45791.1; -

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                                                                             PRINTS; PRO0626; CALRETICULIN.
PROSTIE: PRO01866; CALRETICULIN; 1.
PROSTIE: PSO014: ER_TARGET; 1.
PROSTIE: PSO0803; CALRETICULIN_1; 1.
PROSTIE: PSO0804; CALRETICULIN_2; 1.
PROSTIE: PSO08065; CALRETICULIN_REPEAT; 3.
Endoplasmic reticulum; Calcium_binding; Repeat; Signal.
                                                                                                                                                                                           CALRETICULIN.
G -> A (IN REF. 3).
V -> L (IN REF. 3).
; 65D72C69D0BEC427 CRC64;
                                                                                                                                                                                                                                                                             10.6%; Score 19; DB
100.0%; Pred. No. 6e-
tive 0; Mismatches
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Job time: 118 sec
                                                                                                                                                                                 POTENTIAL
        PIR; A37158; A37158.
FlyBase; EBGN0005585; Crc.
InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_taset.
Pfam; PF00262; calreticulin; 1.
                                                                                                                                                                                                                                      46808 MW;
                                                                                                                                                                                                                                                                                                                                     113 IMFGPDICGPGTKKVHVIF 131
                                                                                                                                                                                                                                                                                                                                                    130 IMFGPDICGPGTKKVHVIF 148
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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107
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size

Searched:

Database :

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN.
Aplysia californica (California sea hare).
Eukaryota, Metazoa, Mollusca, Gastropoda, Opisthobranchia, Anaspidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93098937; PubMed=1463604; Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.; Konnedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.; Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein."; Neuron 9:1013-1024(1992).

EMBL: 55129; AABZ4569:1; -. InterPro; IPR000886; ER_target.

InterPro; IPR0001580; Calreticulin.
                                                                                                                                                                                         Houen G., Koch C.;
"Human placental calreticulin: purification, characterization and association with other proteins.";
Acta Chem. Scand 48:905-911(1994).
InterPro; IPR001580; Calreticulin.
Pfam; PF00262; calreticulin; 3.
Probom; PD001866; Calreticulin; 1.
                                                                              Homo sapiens (Human).
Belarayota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 4; Length 214;
Pred. No. 4e-21;
0; Mismatches 0; Indels
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PRINTS; PR00626; CALRETICULIN;
PRODOSITE: PS00803; CALRETICULIN.;
PROSITE: PS00803; CALRETICULIN.2; 1.
PROSITE: PS00805; CALRETICULIN.2; 1.
PROSITE: PS00805; CALRETICULIN.REPEAT; 3.
PROSITE: PS00014; ER.TARGET; UNKNOWN.1.
SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            AC9269459C1356BE CRC64;
             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN-CALCIUM BINDING PROTEIN (FRAGMENTS).
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Matches 27; Conservative 0;
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60
79
117
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NCBI_TaxID=6500;
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Q26268
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1121.338 Million cell updates/sec
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Q16893 amblyomma a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      091711 xenopus lae
091710 xenopus lae
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Q9u6s0 strongyloce
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                                                                                                                                                                                                      EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180
                                                                                                           ; Search time 23.48 Seconds
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                                                                                                                                                                                                                                                                                                                                                          11
             GenCore.version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        473505 seqs, 146272329 residues
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                                                                                                         January 14, 2002, 08:50:09
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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Match Length
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Gaps

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Gaps

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15.0%; Score 27; DB 5; Length 405; 100.0%; Pred. No. 6.8e-21; ative 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 27; Conservative

214 AA.

PRT;

PRELIMINARY;

**090DG2** 

RESULT Q9UDG2 ID Q9

Score

Result No.

2222227

3 6 7 8 6 11 0 11 0 11 11

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Gaps

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Length 318;

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Query Match 13.9%; Score 25; DB 13; I Best Local Similarity 100.0%; Pred. No. 8.4e-19; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Insect Physiol. 41:369-375(1995)
[2]
SEQUENCE FROM N.A.
TISSUE-SALIVARY GLANDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                              113 IMFGPDICGPGTKKVHVIFNYKGKN 137
ProDom; PD001866; Calreticulin; 1.
                                                                                                                                                           29 IMFGPDICGPGTKKVHVIFNYKGKN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TLVVQFTVKHEQNIDCGGGYVKLF 96
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                                                                                                                                                                                                                                                                                                                   Amblyomma americanum.
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CRT-1.
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Q91711;
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Q91711
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Q16893
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                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryotu; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Susan J.M., Just M.L., Lennarz W.J.;

Susan J.M., Just W.L., Lennarz W.J.;

*Clonding and Characterization of AlphaP Integrin and Calreticulin in Embryos of the Sus Urchin.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF177915; AAD55725.1;

InterPro; IPR000866; ER_target.

InterPro; IPR000868; ER_target.

PRIMTS; PR00262; Calreticulin; 1.

PRINTS; PR00662; CALRETICULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-20063780; PubMed-10594174;
Kuraku S., Hoshiyama D., Kacch K., Suga H., Miyata T.;
"Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
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15.0%; Score 27; DB 5; Length 421;
Begt Local Similarity 100.0%; Pred. No. 7e-21;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      CALRETICULIN,
172C664F59F41F93 CRC64;
                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNW-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA.
                                                                                 421 AA
                                                                                                                                                                                                                                                                                                                                                                ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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111 YNIMFGPDICGPGTKKVHVIFNYKGKN 137
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Interpro; IPR000886; ER_target.
Interpro; IPR001580; Calreticulin.
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CHAIN 20 421
SEQUENCE 421 AA; 48822 MW;
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                                                                                 PRELIMINARY;
                                                                                                                                                                                                       Strongylocentrotus.
NCBI_TaxID-7668;
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Q9PTX7;
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                                                                                 089060
                                                                                              030680
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Q906S0
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TISSUE-SALIVARY GLANDS;
JAWNTSKI D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Amblyomma.
NCBI_TaxID=6943;
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15. TISSUE-SALIVARY GLANDS;
16. Submitted (NOV-1988) to the EMBL/GenBank/DDBJ databases.
17. EMBL; U07708; AAC79094.1;
18. InterPro; IPR001886; ER. target.
18. InterPro; IPR001880; Calreticulin.
19. PR00262, Calreticulin; 1.
19. PRINTS; PR00626; CALRETICULIN.
19. PRODM; PR001886; CALRETICULIN.
19. PROSITE; PS00803; CALRETICULIN.
19. PROSITE; PS00805; CALRETICULIN.
19. PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
19. PROSITE; PS00804; ER. TARGET; UNKNOWN.
10. SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.3%; Score 24; DB 5; Length 410; Best Local Similarity 100.0%; Pred. No. 1.3e-17; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaworski D.C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
016893 PRELIMINARY; PRT; 410 AA. 016893; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-JAN-1999 (TrEMBLrel. 09, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                          163 FTHLYTLIVRPDNTYEVKIDNS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 YNIMFGPDICGPGTKKVHVIF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 YNIMFGPDICGPGTKKVHVIF 131
                          48344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dirofilaria immitis.
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19 3
387 AA;
       13 4
411 AA;
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       CHAIN
SEQUENCE
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN (FRAGMENT).
CALRETICULIN (FRAGMENT).
Eavels (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                   Ireves S., Zorzato F., Pozzan T.;
"Identification of calreticulin isoforms in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treves S., Zorzato F., Pozzan T.; "Identification of calreticulin isoforms in the central nervous
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0
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Pred. No. 1.7e-15;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN.1; 1.
PROSITE; PS00804; CALRETICULIN.2; 1.
PROSITE; PS00805; CALRETICULIN.REPEAT; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00804; CALRETICULIN_REPEAT; 3.
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InterPro; IPR000886; ER_target.
InterPro; IPR001580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 287:579-581(1992).
EMBL, X67598; CAA47867.1; -
InterPro; IPR001580; Calreticulin.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%; Score
v 100.0%; Pre
0, )
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MEDLINE-93074997; Pubmed-1445218;
                                                                                                                                                                                                                                                                           MEDLINE-93074997; PubMed-1445218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 FTHLYTLIVRPDNTYEVKIDNS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 FTHLYTLIVRPDNTYEVKIDNS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00262; calreticulin; 1.
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                                                                                                                                                           Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=8355;
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NON_TER
SEQUENCE
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MEDLINE=9909497; Pubhed=9879888;

MEDLINE=9909497; Pubhed=9879888;

Tauji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;

Tauji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;

Tilarial parasite Dirofilaria immitis.";

Mol. Biochem. Parasitol. 97:69-79(1998).

REMBL; AF052978; AAD03405.1;

REMBL; AF052978; AAD03405.1;

REMBL; PR00262; calreticulin.

Prim; PR00262; calreticulin; 1.

PRINTS; PR00626; Calreticulin; 1.

PRODOR: PR00803; Calreticulin; 1.

PROSTITE; PS000804; CALRETICULIN_2; 1.

PROSTITE; PS000804; CALRETICULIN_2; 1.
                                                                                                                                                            Gaps
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MEDIINE=96234004; PubMed=8654561;
Yamamoto S., Nakamura M.;
Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Ranidae; Rana.
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                                                                                                        Length 411;
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387 CALRETICULIN.
44941 MW; E7741BF6AAFA5885 CRC64;
CALRETICULIN.
891DA66E00EBBEFA CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                        DB 13; I
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                                                                                                  Query Match 12.2%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 22; Conservative 0; Mismatches
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Search completed: January 14, 2002, 08:52:02 Job time: 113 sec
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Onchocarcidae; Litomosoides.
                                                                                                                                                                                        "Strong expression of the calreticulin gene in the liver of Rana rudges Tadboles.";

J. Exp. 2001. 0:0-0(1996).

EMBL; D78589: BAA1425.1;

InterPro; IPR000886; ER_target.
Interpro; IPR001580; Calreticulin.
Pfam; PF00362; calreticulin; I.
PRINTS; PR00626; CALRETICULIN.
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Pred. No. 3e-13;
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Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAL-1 PROTEIN (FRAGMENT).
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100.0%; Pred. No. 3.3e-12;
11ve 0; Mismatches 0;
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PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
SEQUENCE 419 AA; 48658 MW; 2C857036769
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100.0%; Pri
ative 0;
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100.0%; Pre
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FEBS Latt. 387:27-32(1996)
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.

Matches 19; Conservative
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Q90916;
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018478
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DT 01-JAN
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trachesta; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dodo K., Sakoyama Y., Gamo S.;
Dodo K., Sakoyama Y., Gamo S.;
"Drosophila melanogaster calreticulin for mRNA.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO00718; BaA8559.1; -.
RIYBase; FBGN000588; Crc.
InterPro: IPR001880; Calreticulin.
REMINTS: PR00262; calreticulin; 1.
REMINTS: PR00665; Calreticulin; 1.
REMINTS: PR0061866; Calreticulin; 1.
RPOSITE; PS00804; CALRETICULIN.
RPOSITE; PS00804; CALRETICULIN.;
RPOSITE; PS00804; CALRETICULIN.;
RROSITE; PS00804; CALRETICULIN.;
RROSITE; PS00804; CALRETICULIN. REARCH: UNRNOWN. 1.
SEQUENCE 406 AA; 46809 MW; 68BA49A6BBICC427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 19; DB 5; Length 406; 100.0%; Pred. No. 3.5e-12; Live 0; Mismatches 0; Indels
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Best Local Similarity 100..

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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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AAY92351
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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		Description	Human vasostatin (	Recombinant human	60 kD Ro (Ro/SSA)	Human MBP-calretic	Calreticulin. Hom	Calreticulin. Hom	Flea calreticulin	Human secreted pro	Partial sequence o	Castor bean calret	Tories need rotes
		ΩI	_	AAY92350	AAP92276	AAY92349	AAY00927	AAW11156	AAW04171	AAB32385	AAR12312		
		DB	21	77	10	21	20	18	17	21	12	22	22
		Length	180	400	417	417	417	401	403	385	336	415	415
ø₽	Query	Match	100.0	100.0	100.0	100.0	99.5	94.9	72.1	65.0	55.8	54.3	5.4
		Score	971	971	971	971	996	921	200	631	541.5	527	527
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Arabidopsis thalia	Arabidopsis thalla	Arabidopsis thalia	Arabidopsis thalla	Arabidopsis thalla	Arabidopsis thalia	Recombinant human	Recombinant human	Recombinant delta-	A. thaliana enviro	Calnexin sequence.	Recombinant human			Arabidopsis thalia	Zea mays protein f	Arabidopsis thalia	•	Arabidopsis thalia	-		Arabidopsis thalia	Human cClqR bindin	Rat cClqR binding		Arabidopsis thalia	Arabidopsis thalia	Human Endoplasmic	Human prostate can	Human secreted pro	Human secreted pro	Arabidopsis thalia	Arabidopsis thalla	Zea mays protein f
AAG24608	AAG47932	AAG24607	AAG47931	AAG30997	AAG30996	AAY92352	AAY92354	AAY92355	AAY77953	AAR71094	AAY92353	AAG24609	AAG47933	AAG30998	AAG41018	AAG26284	AAG46611	AAG46610	AAB66342	AAG04448	AAG04447	AAY00924	AAY00926	AAY00925	AAG34014	AAG34013	AAB99168	AAB56468	AAG00147	AAG00148	AAG26285	AAG46612	AAG25999
21	21	21	21	21	21	21	21	21	21	16	21	21	21	21	21	21	21	21	22	21	21	70	20	20	21	21	22	21	21	21	21	21	71
421	421	424	424	441	444	61	9	280	417	593	49	312	312	332	84	530	530	267	542	532	548	122	122	122	91	66	256	221	162	162	394	394	125
52.5	52.5	52.5	52.5	52.5	52.5	33.7	32.7	32.7	31.1	29.9	26.6	26.1	26.1	26.1	25.8	24.6		24.6	3.	20.6	ö		19.6	18.7	14.9	14.9			•	•	11.6		11.4
510	510	510	510	510	510	327	318	318	301.5	290	258	253	253	253	250.5	238.5	238.5	238.5	227.5	200.5	200.5	190	σ	œ	4	₹*	140.5			114.5		112.5	110.5
12	13	14	15	16	17	18	19	20	21	22	23	. 24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Inhibiting endothelial cell growth and angiogenesis using calreticulin, MBP-calreticulin; maltose binding protein; vasostatin; N-terminal; angiogenesis; inhibition; endothelial cell; anti-angiogenic; enteroprotective; antidiabetic; cytostatic; dermalogical; hepatic; immunosuppressive; antiinflammatory; anti-atherosclerotic; gastrointestinal; anti-arthritic; ophthalmic. Human vasostatin (calreticulin N-terminal 180 amino acids). (USSH ) US DEPT HEALTH & HUMAN SERVICES. AAY92351 standard; Protein; 180 AA. 99WO-US23240. 98US-0103438 Yao L; (first entry) Pike SE, WPI; 2000-303767/26. WO200020577-A1. Homo sapiens. Synthetic. 05-0CT-1999; 06-OCT-1998; 10-AUG-2000 13-APR-2000. Tosato G, AAY92351;

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23-FEB-1990
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ð
                                                                             contacting the cells with calreticulin (or its fragments).

Fragments of calreticulin causes at least 40% inhibition of anglogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting anglogenesis in a patient. The anglogenesis is ussociated with a disease other than a tumor that is associated with a convecularization (e.g. disbetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, anglofibromas, immune inflammation, atherosciarosis, excessive wound repair, retinal neovascularization, adversary disease, non-immune inflammation, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatical arthitis, systemic lupus erythromatosus, thyroiditis, contact lens averwear, crohn's disease, non-immune inflammation, rheumatical arthitis, systemic lupus erythromatosus, thyroiditis, systemic supus erythromatosus, thyroiditis, and some disease dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBP-calreticulin; maltose binding protein; anglogenesis; inhibition; endothalial cell; anti-anglogenic; neuroprotective; antidiabetic; cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic; anti-atherosclerotic; gastrointestinal; anti-arthritic; ophthalmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SASFEPPSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                             novel method of inhibiting endothelial cell growth comprises
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 971; DB 21;
Pred. No. 3.1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Scott
100.0%; Pred. No. co.
0; Mismatches
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useful for suppressing tumor growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant human MBP-calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92350 standard; Protein; 400 AA
                                Claim 4; Page 82; 99pp; English
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N-PSDB; AAA09346, AAA09347.
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Best Local Similarity 100.
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    180 AA;
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A contraction in see AAY92349 without the IN N-terminal amino acids.

A novel method of inhibiting endothelial cell growth comprises

C contacting the cells with calreticulin (or its fragments/variants).

Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune inflammation, atheroscierosis, excessive wound repair, retinal neovascularization, deference and sees to contact lens overwear, Crohn's disease, non-immune inflammation, nacular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, remained arthifits, systemic lupus erythromatosus, thyroiditis, syndrome, systemic lupus erythromatosus, thyroiditis, syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Inhibiting endothelial cell growth and angiogenesis using calreticulin, useful for suppressing tumor growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                       Recombinant human MBP-calreticulin comprises the sequence of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 971; DB 21;
100.0%; Pred. No. 9.4e-99;
tive 0; Mismatches 0;
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                                                                                                        Claim 4; Page 80-81; 99pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89WO-US01213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma (claimed)
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N-PSDB; AAP92276.
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Best Local Similarity
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Homo saplens
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                                                                                                                                                                 Sequence
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                                           Synthetic peptides corresp. to an epitopic core of Ro antigen are expressed recombinantly to detect autoantibodies, for identification of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241-255. The peptides may be substd. for ribonucleoprotein particle
                                                                                                                                                                                                                                                                                                                                                                             MBP-calreticulin; maltose binding protein; angiogenesis; inhibition; endothelial call; anti-angiogenic; neuroprotective; antidiabetic; cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic; anti-atherosclerotic; gastrointestinal; anti-arthritic; ophthalmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cell growth and angiogenesis using calreticulin,
                                                                                                                                                                                                   61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                               121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                         of Ro 60 kD autoantigen
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                                                                                                                             Length 417;
                                                                                                                                               Indels
A sequences encoding antigenic epitope(s) of Ro (used in immunoassays to detect rheumatic disease
                                                                                                                            100.0%; Score 971; DB 10; 100.0%; Pred. No. 9.9e-99;
                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                suppressing tumor growth
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                             2; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                            Human MBP-calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pike SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-303767/26
                                                                                                                                     Similarity
                                                                                                 417 AA;
                            Disclosure; Fig
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Matches 180;
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                                                                                                  Sequence
                                                                                antigens
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contacting the cells with calreticulin (or its fragments/variants).

Eragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with encovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas, immunue inflammation, atherosclerosis, excessive wound repair, retinal contact lens overwear, Crohn's disease, non-immune inflammation, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis, sociated is syndrome, systemic vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 sasfepfsnkgqtlvvqftvkheqnidcgggyvklfpnsldqtdmhgdseynimfgpdic 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 epavyfkegfldgdgwtsrwleskhksdfgkfvlssgkfygdeekdkglqtsgdarfyal 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
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Pred. No. 9.9e-99;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 180; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 AA;
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08-MAR-1996;
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                    This sequence is calreticulin, a homologue of clq and collectin receptor (cClqR). The invention relates to the use of a cClqR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the cClqR binding domain in a medicament to inhibit cub functionality. The cClqR binding domain, or its inhibitor, can be used to freat a human or animal body. Particularly an inhibitor, is used to complement attuation involved in the initiation and maintenance of inflummation, for example in myocardial infarction, brain isohaemia (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus erythematous, burns, immune complex nephritis, and to treat amyloid plaques in Alzhaimer's diasease. The use of cClqR binding domain or inhibitor, enables the CUB domain functionality to be modulated using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is calreticulin. It and a C-domain derived peptide (AAN06736) are useful for treating a patient to inhibit restenosis. The
                                                                                                                                                                                                                                                                                                                                 121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                          SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of restenosis in patients - using calreticulin or a C-domain polypeptide of calreticulin or a variant with the same
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                                                                                                                                                                                                        Length 417;
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                                                                                                                                                                                                     Score 966; DB 20;
Pred. No. 3.5e-98;
0; Mismatches 1;
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Disclosure; Page 26-27; 31pp; English.
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                                                                                                                                                    ow molecular weight molecule.
                                                                                                                                                                                                      Query Match
Best Local Similarity 99.4%;
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lucas A, Michalak M;
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                                                                                                                                                                       417 AA;
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calreticulin-type opds. are administered either parenterally, intravenously or via a catheter and can target areas of vascular damage to inhibit or prevent restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flea calreticulin protein PCtCall589 (AAW04171) is a calcium-binding protein found in the salivary glands of Ctenocephalides fells. Its amino acid sequence was deduced from a cDNA clone (AAT39516) obtd. from a salivary gland cDNA library. Recombinant PCtCall589 can be produced in host cells transformed with a vector carrying calreticulin nucleic acids. Calreticulin alters the blood feeding behaviour of hematophagous insects and can be administered to an animal to reduce infestation. It reduces calreticulin activity in insects, so reducing the insect burden on an animal. Calreticulin activity and animal to allergic dermatitis caused by fleas, mosquitoes or culicoldes.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haematophagous insect calreticulin protein - used to reduce insect
infestation and desensitise patients to allergic dermatitis
                                                                                                                                                                                                                                                                                                                                       SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC
                                                                                                                                                                                                                                                                                                             1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calreticulin; flea; haematophagous insect; allergic dermatitis;
                                                                                                                                                                                                     Length 401;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                      8
                                                                                                                                                                                               Score 921; DB 18;
Pred. No. 3.1e-93;
                                                                                                                                                                                                                            Pred. No. 3.1e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 68-69; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04171 standard; Protein; 403 AA.
                                                                                                                                                                                               94.9%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US03133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flea calreticulin PCtCal403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; therapy; PctCal403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0401509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                               Query Match 94.9°
Best Local Similarity 95.0°
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rushlow KE, Stiegler GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-442861/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HESK-) HESKA CORP
                                                                                                                 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT39516;
N-PSDB; AAT39517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cytostatic; immunostimulant; antiproliferative; cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer; antipastitc; neuroprotective; nootropic; antimiflammatory; anti-HIV; antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS; autoimmune disease; haematopoletic cell disorder; blood protein disorder; agammaglobulinaemia; hyperproliferative disease; Gaucher's disease; arritythmia; ischaemia; anglogenesis related disorder; Crohn's disease; arrhythmia; ischaemia; anglogenesis related disorder; Crohn's disease; atherosclerosis; neurological disease; Alzheinmer's disease; Huntington's; infectious disease; cat-scratch disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human nucleic acids encoding secreted proteins, useful in the treatment, prevention or diagnosis of immune disorders (e.g. autoimmune diseases), blood protein disorders and hyperproliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore PA;
                                                                                                                                                                                                                                                                      SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                          121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                Gaps
                                                                                                                                                                                                       77
                                                                                                                                                        2 PAVYFKEQFLDGDGWTSRWIESKHK-SDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                  Human secreted protein sequence encoded by gene 15 SEQ ID NO:71.
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                                                                 Length 403;
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                                                                                                                Indels
                                                                                                                  26;
                                                                    DB 17;
                                                                 Score 700; DB 17;
Pred. No. 7.8e-69;
23; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 434-435; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB32385 standard; Protein; 385 AA
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Olsen HS,
                                                               72.1%;
71.7%;
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                                                                                         Best Local Similarity 71.7
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaucher's disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-543578/49
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  403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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  Sequence
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                                                                    Query Match
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ID AAB33485
ID AAB33485
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polynuclectides and polypeptides, or their agonists and antagonists, can be used for treating. proventing or discretization
                                          be used for treating, preventing or diagnosing immune disorders (e.g. cancer, autoimmune diseases), disorders of haematopoietic cells, blood protein disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g. Gaucher's disease), cardiovascular disorders (e.g. congenital heart defects, pulmonary arresia, arrhythmias, ischaemia), angiogenesis related disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases (e.g. AlDS, cart-scratch disease and other bacterial, viral, parasitic or fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 vyfqeefldgehwrnrwlgstndsrfghfrlssgkfyghkekdkglqttqngrfyaisar 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 FEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               River blindness; onchocerciasis; vaccine; antigen; parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial sequence of Onchocera volvulus 42 kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 631; DB 21;
llarity 64.4%; Pred. No. 3e-61;
Conservative 30; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160..166
/label= repeat unit
/note= "hydrophilic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195..201
/label- repeat unit
/note= "hydrophilic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= repeat unit
/note= "hydrophilic"
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ID AAR12312 standard; Protein; 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greene BM, Unnasch TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-185179/25.
N-PSDB; AAQ11987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 114; Conser
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                                                                                                                                                                                                                                                                                                                                                           385
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                                                                                                                                                                                                                                                                                                         Invention
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                                                                                 The sequence was deduced from a cDNA clone lambda RAL-1 prepd.

from RNA isolated from nodules excised from patients infected
with 0. volvulus. The N-terminal is incomplete, however Abs
which specifically bind to protein prepd. from induced cultures
of lambda RAL-1 lysogens recognise a single polypeptide of mol.
wt. 42.000 in extracts of adult worms. Analysis deduced sequence
suggests that it encodes a protein of mol. wt. 39,130. If the
antigen is not subject to post-translational processing this
suggests that most of the coding sequence is present. The three
crepeats are highly hydrophilic regions likely to be exposed on
the surface of the antigen and highly immunogenic. Recombinant
antigen expressed by the clone can be used stimulate T-cells of
individuals infected by the parasite to proliferate and may be
used as the basis for a vaccine against Onchocerciasis or river
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSLDQTDMHGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 FYGDEEKDKGLQTSQDARFYALSASFE-PFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFP 97
 DNA encoding Onchocerca volvulos antigen – used to express recombinant antigen for vaccine against onchocerciasis or river
                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                   55.8%; Score 541.5; DB 12;
68.5%; Pred. No. 1.9e-51;
11ve 21; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castor bean calreticulin SEQ ID NO: 2.
                                                            Disclosure; Fig 7; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 IVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66341 standard; Protein; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calnexin; promoter; resistance.
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Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                        336 AA;
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                               blindness.
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                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                  The present invention provides the protein and coding sequences for the castor bean calreticulin protein and the calreticulin promoter sequence. In addition, the castor bean calnexin protein, coding sequence and promoter are also described. Calreticulin and calnexin are calcium binding proteins found in the endoplasmic reticulum (er). The calreticulin promoter sequence can be used in vectors to promote the expression of foreign genes, particularly resistance genes, in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding a calcium binding chaperone protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum; calnexin; promoter; resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
in endoplasmic reticulum, calreticulin, and calreticulin promoter sequences, useful for producing foreign gene products in plant cells
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                     4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
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                                                                                                                                                                                                                                                                                                                                    43; Indels
                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                  54.3%; Score 527; DB 23
55.3%; Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66343 standard; Protein; 415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1B; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
                                                 Claim 1; Fig 3; 45pp; English.
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                    SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
promoter are also described. Calreticulin and calnexin are calcium binding proteins found in the endoplasmic reticulum (er). The calreticulin promoter sequence can be used in vectors to promote the expression of foreign genes, particularly resistance genes, in plant
                                                                                                               Gaps
                                                                                                                                           121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                               4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                           .,
                                                                                        Length 415;
                                                                                                             43; Indels
                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 28350.
                                                                                       54.3%; Score 527; DB 22; 55.3%; Pred. No. 1e-49;
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990S-0126785.
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                                                                                    Query Match
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07-MAY-1999;
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                                                                                                                                                                                         52.5%; Score 510; DB 21;
53.9%; Pred. No. 7.8e-48;
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nes 97; Conservative
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promoter;
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99US-0161404
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Matches 97; Conservative
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25-OCT-1999;
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06-APR-1999;
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Search completed: January 9, 2002, 15:01:12 Job time: 158 sec

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Sequence Sequence Sequence

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Patent No. 6171804

Patent No. 6171804

APLICANT: Coughlan, Sean J.

APLICANT: Winfrey, Jr., Ron J.

APLICANT: Winfrey, Jr., Ron J.

APLICANT: Winfrey, Jr., Ron J.

TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND UNDERSED OF SEQUENCES: 16

CORRESPONDENCE ADDRESS: 16

CORRESPONDENCE Seed and Berry

STRATE: Washington

COUNTRY: U.S.A.

ZIP: 98104-7092

COMPUTER READABLE FORD:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: BENDABLE FORD:

APPLICATION NUMBER: NS/08/675,816

FILING DATE: 05-01L-1996

CLARSTRICATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 750027.401

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 415 amino acids

TYPE INDRESSED COMPUTER:

TOTAL COMPUTER: 100 acids

TELENTER: 100 acids

TOTAL COMPUTER: 100 acids

TOTAL COMPUTER: 100 acids

TELENTER: 100 acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VFFEERF--EDGWENRWVKSDWKKDENTAGEWNYTSGKWNGD-PNDKGIQTSEDYRFYAI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.3%; Score 527; DB 4; Length 415; 55.3%; Pred. No. 2e-51; tive 31; Mismatches 43; Indels
                            US-08-460-736-120
US-08-480-604A-10
US-08-405-496A-10
US-08-915-136-10
US-08-946-914-11
US-08-473-553A-5
US-08-245-511-47
US-08-245-511-47
US-08-245-511-47
US-08-245-511-47
                                                                                                                                                                                                                       US-07-906-397A-2
US-08-601-891-2
US-09-021-324-2
                                                                                                                                                                         US-07-977-451-2
US-07-946-507-2
US-08-252-517-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.3%
Matches 99; Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2
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                                                                                                                             (without alignments)
105.649 Million cell updates/sec
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Sequence 8, Appli
Sequence 8, Appli
Sequence 48, Appli
Sequence 53, Appli
Sequence 5, Appli
Sequence 56, Appli
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                                                                                                                                                                                                      1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 18C
                                                                                                          ; Search time 38.34 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-181-706-8

US-09-458-791-8

US-08-600-993A-48

US-08-991-408-4

US-08-991-408-5

US-08-991-408-7

US-08-991-408-7

US-08-991-408-2

US-08-991-408-2

US-08-240-473-5

US-08-240-473-5

US-08-240-473-5

US-08-240-473-5

US-08-240-473-5

US-08-240-473-5

US-08-240-473-5

US-08-940-086A-56

US-08-940-086A-56

US-08-940-086A-56

US-08-940-046A-20

US-08-940-04A-20

US-08-940-04A-20

US-08-940-04A-21

US-08-940-04A-21
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                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
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                                                                                                         January 9, 2002, 14:58:33
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Maximum Match 100%
Listing first 45 summaries
                                                                            protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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971
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Match Length
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Perfect score:
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RESULT 3
US-08-675-816-6
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                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
TITLE OF INVENTION: PROTEIN PRODUCTION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ئ</u>
53 QDARFYALSASF-EPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPN----SLDQTDMHG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 DSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCK-------DDEFTHLYTL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                        4 VYFKEQFLDGDGWTSRWIESKHKSD-----FGKFVLSSGKFYGDEEK------DKGLQTS 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.9%; Score 290; DB 1; Length 593; 38.1%; Pred. No. 2.1e-24; tive 26; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NOTE:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37,120
FR: 690066.401C1
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Patent No. 5691306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 IVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                                                                    APPLICANT: Bergeron, John J.M. APPLICANT: Thomas, David Y. APPLICANT: Wada, Ikuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bost Local Similarity 38.19
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-296-362-2
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: Washington
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                                                                                                                             US-08-296-362-2
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APPLICANT: Coughlan, Sean J.
APPLICANT: Winfrey, Jr., Ron J.
TITLE OF INVENTION: CARRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSASF- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 PGTKKVHVIFNYKG--KNVLINKDIR----CKDDEFTHLYTLIVRPDNTYEVKIDNSQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Melanie K. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEARPHORIN PROFEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
TORRESPONDENCES:
ADDRESSE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.4%; Score 227.5; DB 436.0%; Pred. No. 2.2e-17, Live 24; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: No. 6171864 tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:
TELEFAX: (206,522-4900
TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
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Patent No. 6130068
; Sequence 6, Application US/08675816
; Patent No. 6171864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.0
Matches 64; Conservative
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                                            GENERAL INFORMATION:
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COUNTRY: U
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US-09-459-066-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YKGKNVLINKDIRCKDDEFTHLYTLIVRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YFKEQFLDGDGWTSRWIESKHKSDFGKFVLS---SGKFYGDEEKDKGLQTSQDARFYALS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                        APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 660;
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GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 89; DB 4;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 41; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09458791
Patent No. 6174689
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/ACENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 660 amino acid
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609 NTIYSFDTKSKQTRSAQVD 627
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206)470-4189
(206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-181-706-8
                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 PGTKKV-HVIFN----
98101
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US-09-458-791-8
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| : |: :| | : | | 448 YIAQMCLNDEGGPSS-LSSHRWSTFLKVELECDIDGRSYRQIIHSKAIKTDNDTLLYVFF 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YKGKNVLINKDIRCKDDEFTHLYTLIVRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YFKEQFLDGDGWTSRWIESKHKSDFGKFVLS---SGKFYGDEEKDKGLQTSQDARFYALS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.2%; Score 89; DB 4; Length 660; 20.6%; Pred. No. 0.14; tive 25; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Henry, Janis C

REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRATING SYSTEM: MS-DOS/Windows 95
OPFTWARE: Word for Windows 95, 7.0a
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2631
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)333-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09459066
; Patent No. 6187909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 661 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609 NTIYSFDTKSKOTRSAQVD 627
ZIP: 98101
COMPUTER READABLE FORM:
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Best Local Similarity 20.6%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 PGTKKV-HVIFN-----
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MEDIUM TYPE: Floppy
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; PAGES: 633-
; DATE: 1990
US-08-245-511-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 YIAQMCLNDEGGPSS-LSSHRWSTFLKVELECDIDGRSYRQIIHSKAIKTDNDTILYVFF 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 PGTKKV-HVIFN--------YGKNVLINKDIRCKDDEFTHLYTLIVRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YFKEQFLDGDGWTSRWIESKHKSDFCKFVLS---SGKFYGDEEKDKGLQTSQDARFYALS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 89; DB 4; Length 660; Best Local Similarity 20.6%; Pred. No. 0.14; Matches 41; Conservative 25; Mismatches 91; Indele
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Serons A. S. 5928900

GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JULIANTE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
NROR ASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
                    APPLICATION NUMBER: US/09/459,066
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  NAME: HGDLY, JGDIS C
REGISTRATION NUMBER: 34,347
REPRENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEPAX: (206)423-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 DNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609 NTIYSFDTKSKQTRSAQVD 627
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                       umino acid
GY: linear
                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-245-511-48
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sequence error; the correct sequence shown below is obtain from \operatorname{GENBANK}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 EPFSNKGQTLVVQFTVKH-----EQNIDCGG-GYVKLFPNSLDQT---DMHGDSEY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 EQYWDKENVHLDTINLAYYDGSDQESLERNFTSGAYSYARLYPTSSNYSKVAEEYKDNIY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 YTQSGSGIAGLGVNIDRQSYNYTSKTTDSEKVATKKALLINKDFRQALNFALDRSAYSAQI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 WTSR-----W----IESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSASF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0%; Score 77.5; DB 2; Length 642; Best Local Similarity 21.2%; Pred. No. 2.6; Matches 42; Conservative 20; Mismatches 81; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 NIMFGPDICGPGTKKVHVIFNYKG------KNVLINKDIR----
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Patent No. 5981229
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                      NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 6001-069 CIP
TELECOMUNICATION INFORMATION:
TELEPRONE: 201 487-5800
TELEPRONE: 201 343-1684
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
CLONE: amia
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STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 -CKDDEFTHLYTLIVRPD 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Alloing, et al.
JOURNAL: Mol. Microbiol.
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633-644
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CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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  GENERAL INFORMATION:
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STATE: PA
COUNTRY: USA
TO: 19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-991-408-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 NIMFGPDICGPGTKKVHVIFNYKG------1KNVLINKDIR------145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 WTSR-----W----IESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSASF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%; Score 77.5; DB 2; Length 642; Best Local Similarity 21.2%; Pred. No. 2.6; Matches 42; Conservative 20; Mismatches 81; Indels 55;
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                 PULBASJELICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION ATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY OBJEC: 01-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Jackson ESq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 US
TELEPHONE: 201 487-5800
TELEPAN: 201 487-5801
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LEMETHY OF SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
CLONE: amiA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-946-026-53
; Sequence 53, Application US/08946026
; Patent No. 6034118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 642 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 -CKDDEFTHLYTLIVRPD 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Alloing, et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL: Mol. Microbiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-600-993A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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Gaps
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Witcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 77; DB 3; Length 15; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ARLETH, ANTHONY J.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
ITTLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
ITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: RATHER & PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-0CT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKL, DAVId J.
REFERENCE/POCKET NUMBER: 210121.424C1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08991408
Patent No. 6008017
                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 981.04-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.9
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PAVYFKEQFLDGDG 15
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68 SNKGQTLVVQF-TVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG-TK 125
                                                                                                                                                                                                                                                                       68 SNKGQTLVVQF-TVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG-TK 125
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                            DB 2; Length 1013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1013;
                                                                                                                                                            Query Match 7.7%; Score 75; DB 2; Length 1013
Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                                                                                                                        973 EIYSI----GDSVLIHFHTDDTINKKGFHIRYKSIRYPDTTHTKK 1013
                                                                                                                                                                                                                                                                                                                                     126 KVHVIFNYKGKNVLI -- NKDIRCKDDEFTHLYTLIVRPDNTYEVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Takahara, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
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Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches
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APPLICATION NUMBER: US/09/021,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09021287
Patent No. 5981717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
  LENGTH: 1013 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                ; MOLECULE TYPE: protein US-08-866-650-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-021-287-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Mad
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-021-287-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.7%; Score 75; DB 3; Length 591; Best Local Similarity 31.4%; Pred. No. 4.5; Mutches 33; Conservative 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 KVHVIFNYKGKNVLI--NKDIRCKDDEFTHLYTLIVRPDNTYEVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 EIYSI----GDSVLIHFHTDDTINKKGFHIRYKSIRYPDTHTKK 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Borson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                          ATG-50038
                                           FILING LAID.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-50(
TELEPONGET: 610-407-0701
TELEPONGET: 610-407-0701
TELEFAK: 610-407-0701
TELEFAK: 846169
INFORMATION FOR SEG ID NO: 4:
SENDIENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quarles & Brady
South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08866650; Patent No. 593931; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-08-866-650-5
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g ð 8 Takahara, Kazuhiko

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68 SNKGQTLVVQF-TVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG-TK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 75; DB 3; Length 1013; ; Pred. No. 9.7; 15; Mismatches 39; Indels
                                                                                                                                                                                                                  APPLICANT: ALECTH, ANTHONY J.
APPLICANT: ALECTH, ANTHONY J.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
ADDRESSEE: RATHER & PRESTIA
STREET: P.O. BOX 980
                            973 EIYSI----GDSVLIHFHTDDTINKKGFHIRYKSIRYPDTHTKK 1013
126 KVHVIFNYKGKNVLI--NKDIRCKDDEFTHLYTLIVRPDNTYEVK 168
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,408
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATG-50038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAULF
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-5003
TELEPHONE: 610-407-0700
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION OF SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence 5, Application US/09240473; Sequence 5, Application US/09240473; Patent No. 6297011 GENERAL INFORMATION: APPLICANT: Greenspan, Daniel S
                                                                                                                                                       Sequence 2, Application US/08991408 Patent No. 6008017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%;
Best Local Similarity 31.4%;
Matches 33; Conservative 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ARLETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-991-408-2
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Sequence 56 Application US/08231193A
Patent No. 584895
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Elis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 SNKGQTLVVQF-TVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPG-TK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KVHVIFNYKGKNVLI--NKDIRCKDDEFTHLYTLIVRPDNTYEVK 168
APPLICANT: Hoffman, Guy G
TTLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 AURENT APPLICATION DATA:
AURLICATION NUMBER: US/09/240,473 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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Best Local Similarity 31.4%; Pred. No. 9.7;
Matches 33; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960296.93839
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDUIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELERAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1013 amino acids
                                                                                                                                                                                  COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-240-473-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                    STATE: WT
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY FACENT INFORMATION:
NAME: SAIdman, Stephanie
REGISTRATION NUMBER: 6362-9383
FELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0969
INFORMATION POR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-193A-56
```

Query Match 7.5%; Score 72.5; DB 2; Length 1484; Best Local Similarity 27.7%; Pred. No. 32; Matches 23; Conservative 13; Mismatches 28; Indels 19; Gaps

100 L------DQTDMHGDSEY 111

õ

Search completed: January 9, 2002, 14:59:42 Job time: 69 sec

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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

Run on:

9, 2002, 14:58:53 January

; Search time 43.73 Seconds
(without alignments)
313.547 Million cell updates/sec

US-09-828-000-3

971 1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

219241

219241 seqs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\* 1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	calreticulin precu			calreticulin,	calreticulin	calreticulin	calreticulin	calreticulin	calreticulin	calreticulin	calreticuli	41K larval an	calreticuli	calreticulin - bar	calreticulin precu	calreticulin		calreticulin	calreticulin	calreticulin		hypothetical prote	ılin	probable calreticu	calnexin precursor	calnexin	calnexin	calnexin precursor	
SUM	ΩI	A37047	JH0819	A34154	S43376	806763	S29129	JH0795	S29130	S71343	A56637	S25851	A32507	T05703	T05705	S58170	T14554	T10172	836799	T16968	T03691	C36605	H86224	A48573	T07841	B54354	C54354	I53260	A37273	1
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	Query Match Length	417			400			405																		591	591	592	593	503
đ	Query	100.0	96.1	95.9	95.8	95.8	96.0	82	82	82	72	63	55	55	55	55	54	54	23	53	53	22	52	21	35			29.9		
	Score	971	933	931	930	930	835	804	797	196	669	619.5	542.5	539	539	536	531	527	522.5	522	517	512	510	496	347	293	290	290	290	200
	Result No.	-	7	က	4	ഗ	9	7	<b>&amp;</b>	σ	10	11	12	13	14	15	,16	17	18	19	20	21	22	23	24	25	26	27	28	20

calmegin precursor	calcium-binding pr	calnexin-t - mouse	calnexin homolog S	hypothetical prote	calnexin-like prot	calnexin - soybean	probable calnexin	calnexin homolog -	calreticulin, uter	calreticulin, slow	calreticulin, brai	calnexin homolog Y	calnexin homolog C	calnexin - maize (
A53418 S71342	S56142	A54086	A46637	S40938	JN0597	T06415	T10892	T49873	E33208	C33208	D33208	S29347	S70552	T03251
2 2	10	~	~	~	7	~	7	7	N	7	~	~	7	7
611	560	611	582	619	530	546	540	532	58	59	29	502	297	428
27.8	26.1	26.0	25.5	25.1	24.6	23.9	22.2	20.6	16.2	14.9	14.8	13.7	13.3	12.8
270	253.5	252	248	244	238.5	232	215.5	200.5	157	145	144	133.5	129	124.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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A37047 Laterate names: SAK ribonocleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr calreticuln precursor - human
Nalternate names: SAK ribonocleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr C;Species: Homo sapplems (man)
C;Date: 10-Sep-199 sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C;Date: 10-Sep-199 #text_change 18-Feb-2000
A;Hite: The SP-5-1562, 1992
A;Hite: The SP-5-1562
A;Hite: The SP-5-162
A;H
```

A; Molecule type: protein A; Residues: 18-27 < DUP>

A:Experimental source: LAK cell
R;Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A;Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

us-09-828-000-3.rpr

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A; Molecule type: protein
A; Residues: 18-36 <VAN>
R; Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Blochem. J. 271, 473-480, 1990
A; Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A; Reference number: S13045, MUID:91054414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 'R', 270-358,'AAG' <LON>
A; Residues: 'R', 270-358,'AAG' <LON>
A; Residues: 'R', 270-358,'AAG' <LON>
A; Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
B; Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A; Title: Identification of protein disulfide isomerase and calreticulin as autoimmune
A; Reference number: S39371; MUID:94072621
R.Murthy, K.R.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel Nucleic Acids Res. 18, 4933, 1990
A.Title: Structural homology between the rat calreticulin gene product and the Onchoc A; Reference number: S11205; MUD:90370496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: testis, strain Sprague-Dawley R; Sconnatchsen, B.; Fuellekrug, J.; Wan Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies submitted to the EMBL Data Library, May 1994.
A; Description: Retention and retrieval: both mechanisms cooperate to maintain calreti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Wolecule type: protein
A;Realdues: 18-23, XY, 25-32 (YOK>
A;Realdues: 18-23, XY, 25-32 (YOK>
J. Biol. Chem. 264, 17494-17501, 1989
A;Title: Four intracalsternal calcium-binding glycoproteins from rat liver microsomes little: Pour intracalsterning rat liver vesicles.
A;Reference number: A34473; MUID:90008920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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A; Residues: 1-416 < MUR.
A; Residues: 1-416 < MUR.
A; Residues: 1-416 < MUR.
A; Cross-references: EMBL. X53363; NID:955854; PIDN:CAA37446.1; PID:955855
A; Cross-references: EMBL. X: Baba, T.; Okinaga, S.; Arai, K.
Biochem. Blophys. Res. Commun. 186, 668-673, 1992
A; Title: Calreticulin is present in the acrosome of spermatids of rat testis.
A; Reference number: PCI109; MUID:92360010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-416 <SOE>
A;Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:1-17/Domain: signal sequence *status predicted <SIG>F:18-416/Product: calreticulin *status experimental <MAT>F:204-212/Region: nuclear location signal F:413-416/Region: endoplasmic reticulum retention signal F:344/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
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Pred. No. 8.8e-77;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricone, Y.C.; Bailly, A.; Latruffe, N. submitted to the EMBL Data Library, December 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: calreticulin
C; Keywords: calcium binding; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.1%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 18-32 <NAK2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 18-29 <TRE>
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
B; Raesidues: 18-32 KKRA-
K; Lemens: 18-32 KKRA-
K; Lemens: 18-32 KKRA-
Bubmitted to the EMBL Data Library, November 1996
A; Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regic
A; Reference number: 22906
A; Reference number: 22906
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                     A; Molecule type: protein
A; Residues: 18-34,'R' <ROJ>
K; Rause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A; Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif A; Reference number: S11475; MUID:90380058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C; Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C; Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
C; Accession: JH0819; A49176; J1205; PMichikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S. Exp. Coll Res. 205, 101-110, 1993
Exp. Coll Res. 205, 101-110, 1993
A; Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom A; Accession: JH0819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: cell line 5HL2-B; fibroblast C; Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and
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A; Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572
A; Accession: A49176
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A;Regidues: 1-416 <NA2>
A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAAll345.1; PID:g1845572
A;Experimental source: Sprague-Dawley, spermatogenic cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-rrferences: GDB:125179; OMIM:109091
A; Mup position: 19p13.3-19p13.2
A; Introne: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-17/Domain: signal sequence #status predicted <SIG>F;18-417/Product: calreticulin #status predicted <MAT>F;414-417/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-417 <LAM>
A; Cross-references: EMBL: AD000092; PIDN: AAB51176.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keywords: calcium binding; integrin binding
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N;Altornate names: calcium-binding protein 3
                                                      Reference number: A40346; MUID:92002034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: calreticulin
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                                                                                       Accession: A40346
                                                                                                                                                                                                                                                                                                                                     A; Accession: S11475
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Matches 180;
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A Accession: JC1444
A; Molecule type: mRNA
Residues: 1-416 AMAL>
A; Cross-references: GB: M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
A; Accession: PC1233
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 18-41 AMAL>
B; White, T.K.; Zhu, Q.; Tanzer, M.L.
A; Relidues: 18-10 Chem. 270, 18926-15929, 1995
A; Title: Cell surface calreticulin is a putative mannoside lectin which triggers mous A; Reference number: A57498; MUID:95332280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca A; Reference number: JC1444; MUID:93013037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calreticulin (CRP55, calregulin, HACBP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06763; JC1444; PC1233; A57498
R;Smith, M.J; Roch, G.L.E.
BENBO J. 8, 3581-3586, 1989
A;Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, A;Reference number: S06763; MUID:90059955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SARFEPPSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPAGLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPNNTYEVKIDNSQVESGSLE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X14926; NID:q50567; PIDN:CAA33053.1; PID:q50568 R;Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M. Green, M. Geen 120, 217-225, 1992
                A.Katus: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 45-63, °E', 65-83 <LIU>
A.Residues: 45-63, °E', 65-83 <LIU>
A.Experimental source: brain, clone 8.1
C.Superfamily: calreticulin
C.Superfamily: calcium binding; glycoprotein
F.397-400/Region: endoplasmic reticulum retention signal
F.120-146/Disulfide bonds: #status experimental
F.162/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: 55K calcium-binding reticuloplasmin; calregulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 930; DB 1; Length 416;
Pred. No. 1.6e-76;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length 400
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.8%; Score 930; DB 2; L
Best Local Similarity 95.0%; Pred. No. 1.6e-76;
Matches 171; Conservative 3; Mismatches 6;
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A;Residues: 74-80;142-151;186-193
C;Superfamily: calreticulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.8%;
Best Local Similarity 94.4%;
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-416 <SMI>
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A; Accession: S36801
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R;Treves, S.; de Mattel, M.; Lanfredl, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Blochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: brain
R; Liu, N.; Fine, R.E.; Johnson, R.J.
Bicchim. Biophys. Acta 1202, 70-76, 1993
A; Title: Comparison of cDRAs from bovine brain coding for two isoforms of calreticulin.
A; Reference number: S36799; MUID:93385184
                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34154; S13047
R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Balo, Chem. 264, 21522-21589 1989
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)
A;Reference number: A34154; MUID:90094320
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S43376
calreticulin, brain isoform 1 - bovine
CiSpecies: Bos primigentus taurus (cattle)
CiSpecies: 20-oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
CiSpecies: X1376; S36801
R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T. Blochem. J. 298, 435-442, 1994
A;Title: Covalent structure of bovine brain calreticulin.
A;Reference number: S43376; MUID:94183174
                           SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                      121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                         138 GPGTKKVHVIENYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197
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F;1-17/Domain: signal sequence #status predicted <SIG>
F;415-418/Region: endoplasmic reticulum retention signal
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Pred. No. 1.3e-76;
1; Mismatches 7
                                                                                                                                                                                                                                                                                                                RESULT 3
A34154
calreticulin precursor, skeletal muscle
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Best Local Similarity 95.6%;
Matches 172; Conservative
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A, Molecule type: protein
A, Residues: 1-400 <MAT>
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A; Molecule type: protein
A; Residues: 19-32 <TRE>
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A; Residues: 1-418 <FLI>
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Cyspecies: Xenopus laevis (African clawed irog) (Iragment)
Cyspecies: Xenopus laevis (African clawed frog)
Cybate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
Cybate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
Cybates: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
Cybates: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
RyTreves S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A; Title: Identification of calreticulin isoforms in the central nervous system.
A; Reference number: S29129; MUID:93074997
A; Reference: EMBL:X67598
A; Residues: 1-384 cTRE>
A; Accession: Toll068
A; Residues: 1-389, XYGRY CTRM>
A; Residues: 1-399, XYGRY CTRM>
A; Residues: 1-339, XYGRY CTRM>
A; Residues: 1-330, XYGRY CTRM>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DGDGWTQRWYESKHKSDYGKFKLSAGKFYGDSEKDKGLQTSQDARFYAMSSRFESFSNKD 60
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A; Experimental source: CNS
C; Superfamily: calreticulin
C; Keywords: glycoprotein
F; 381-384/Region: endoplasmic reticulum retention signal
F; 381-386/Binding site: carbohydrate (Asn) (covalent) #status predicted
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85.2%; Pred. No. 1.6e-64;
iive 12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 804; DB 1; 79.4%; Pred. No. 3.9e-65; tive 18; Mismatches 17
A; Reference number: A94207; MUID:88320566
A; Accession: B31409
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Best Local Similarity 85.29
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 143; Conservative
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Best Local Similarity
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A; Rosiduae: 1.405 AKEN>
A; Rosiduae: 1.405 AKEN>
A; Cross-references: 1.405 A; Experimental source: 1.405 B; Commody T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
A; Title: Squencing of proteins from two-dimensional gels by using in situ digestion and tion in Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Long-term sensitization training in aplysia leads to an increase in calreticuli
A;Reference number: JH0795; MUID:93098937
A;Accession: JH0795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
s29129
calrettuin precursor (clone 3) - African clawed frog (fragment)
C; Species: Xenopus leavis (African clawed frog)
C; Species: Xenopus leavis (African clawed frog)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C; Accession: 539129
R; Treves, S; 2orzato, F; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A; Title: Identification of calreticulin isoforms in the central nervous system. A; Reference number: S29129; MUID:93074997
A; Riceis in Internation of Calreticulin isoforms in the central nervous system. A; Recession: S29129
A; Rociosion: Riceir Calreticulin for Status predicted (SIG)
F; 1-12/Domain: S1gnal sequence (fragment) #status predicted
F; 13-41/Product: Calreticulin for Status predicted
F; 339/Binding site: Carbohydrate (Asn) (covalent) #status predicted
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JH0795
Calrettculin precursor - California sea hare
N;Alternate names: protein 407
C;Species: Aplysia californica (California sea hare)
C;Bate: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999
C;Accession: JH0795; B31409; F60977
R;Kennedy, T.E.; Kuhl, D.; Barzllai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                             121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                 18 DPAIYFKEQFLDGDAWINRWVESKHKSDFGKFVLSSGKFYGDLEKDKGLQTSQDARFYAL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLS$GKFYGDEEKDKGLQTSQDARFYAL 60
                                  1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutches 151; Conservative
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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Saccession: $25851; T33996
F.Smitch, M.J.
DNA Seq. 2, 235-240, 1992
A;Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A;Reference number: $25851; MUID:92329978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A;Experimental source: strain Bristol N2; clone Y38A10A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEXNIMFGPDICGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FE-PFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDKDFSNKGKTLVIQYTVKHEQGIDCGGGYVKVMRADADLGDFHGETPYNVMFGPDICGP 135
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                     17 VYFKEEFNDA-SWEKRWVQSKHKDDFGAFKLSAGKFFDVESRDQGIQTSQDAKFYSRAAK 75
                                                                                                                                                                                                                                                                                                                       4 VYFKEQFLDGDGWTSRWIESKHK-SDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
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                                                                                                                                                                                                      Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1;
R;Bauer, C.; Courtney, L.; LaPlant, Y.
submitted to the EMBL Data Library, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 1077.3; 315/3
C;Superfamily: calreticulin
F;1-15/Domain: signal sequence #status predicted <SIG>
F;392-395/Region: endoplasmic reticulum retention signal
  A;Introns: 65/1; 222/3
C;Superfamily: calreticulin
C;Reywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F;403-406/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: The sequence of C. elegans cosmid Y38A10A
A;Reference number: Z21453
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63.5%; Pred. No. 1.8e-48;
ive 26; Mismatches 36;
                                                                                                                                                                                                   Score 699; DB 2;
Pred. No. 1.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-395 <BAU>
                                                                                                                                                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calreticulin precursor - Caenorhabditis elegans
                                                                                                                                                                                                   72.0%; Score 699; 74.2%; Pred. No. 1
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: Y38A10A.5
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Best Local Simi
Matches 113;
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Matches 132;
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Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIF:128275)
R;McCaullife, D.P.; Zappi, E.: Lieu, T.S.; Michalak, M.; Sonthelmer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A;Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly homony. Reference number: A37158; MUID:90307981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Seq. 3, 247-250, 1992
A;Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin
A;Reference number: A56637; MUID:93208374
A;Accession: A56637
                                                                                                                                                                                                                                                                                                                                                                                Rana
                                                                                                                                                                                                                                                                                                                                                                          the frog,
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C;Superfamily: calreticulin
C;Keywords: calculin binding; endoplasmic reticulum
F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C;Species: Drosophila melanogaster
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C;Accession: A56637; A37158
                                                                                                                                                                                                                           C;Species: Rana rugosa (Korean frog)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
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132 NYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                OYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSLE 169
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WCC
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                                                                                                                                                                                                                                                                              C; Accession: S71343
R; Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A; Title: Calnexin: its molecular cloning and expanded and an experimental and expension: S71342; MUD:96234004
A; Reference number: S71342; MUD:96234004
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-419 < YAM>
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                                                                                                                                                                                                 calreticulin precursor - Korean frog
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Matches 145; Conserv
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A; Residues: 1-406 <SMI>
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-421 < CDRE>
A; Residues: 1-421 < CDRE>
A; Cross-references: EMBL: X89813; NID: 9927571; PIDN: CAA61939.1; PID: 9927572
B; Napier, R.M.; Trueman, S.; Henderson, J.; Boyce, J.M.; Hawes, C.R.; Fricker, M.D.; Submitted to the EMBL. Data Library, November 1994
A; Description: Purification and sequencing of calreticulin from maize and evidence for A; Reference number: $49818
                                                                                                                       R;Chen, F;; Hayes, P.M.; Mulroony, D.; Pan, A.
Plant Cell 6, 835-843, 1994
A;Title: Identification and characterization of cDNA clones encoding plant calreticul
A;Reference number: 215422; MUID:94339696
A;Accession: T05705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S58170; S49818
R;Dresselhaus, T.; Hagel, C.; Loerz, H.; Kranz, B.
submitted to the EMBL Data Library, July 1995
A;Description: Isolation of a CDNA encoding Calreticulin from in vitro zygotes of mai A;Reference number: S58170
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calreticulin - barley (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T05705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Zea mays (maize)
C;Date: 13-Jan_1996 #sequence_revision 01-Mar-1996 #text_change 13-Aug-1999
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A;Molecule type: DNA
A;Rosidues: 1-41 <NAP>
A;Ross-references: EMBL:246772; NID:q577611; PIDN:CAA86728.1; PID:q577612
                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mannA
A;Residues: 1-415 <CHE>
A;Cross-references: EMBL:L27349; NID:g439587; PIDN:AAA32949.1; PID:g439588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
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C; Keywords: calculum binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;1-8-421/Region: endoplasmic reticulum retention signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: cv. Morex, ovary C; Genetics:
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C; Superfamily: calreticulin
C; Keywords: calcium binding
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Plant Cell 6, 835-843, 1994
A/Title: Identification and characterization of cDNA clones encoding plant calreticulin A/Recension: T05703
A/Accession: T05703
A/Status: preliminary; translated from GB/EMBL/DDBJ
                         C; Species: Onchocerce volvulus
C; Date: 12. May-1990 #text_change 12-Apr-1995
C; Date: 12. May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C; Accession: A,22507; A,28813
R; Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
J. Cilin. Invest: 82, 252-269, 1988
A; Tille: Isolation and characterization of expression cDNA clones encoding antigens of A; Reference number: A92769; MUID:88273584
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Calreticulin - barley (fragment)
C;8pcies: Hordeum vulgare (barley)
C;Dute: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
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41K larval antigen - nematode (Onchocerca volvulus) (fragment)
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68.5%; Pred. No. 1.3e-41;
ilve 22; Mismatches 22
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C; Superfamily: calreticulin
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A; Molecule type: mRNA
A; Residues: 1-336 <UNN>
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A; Residues: 1-412 <CHE>
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C; Superfamily: calr
C; Køywords: calcium
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Matches 101;
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Query Match 55.2%; Score 536; DB 2; Length 421; Best Local Similarity 56.4%; Pred. No. 6.7e-41; Matches 101; Conservative 31; Mismatches 41; Indels
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61 SASEEPESNKGOTI.VVOETVKHEONIDGGGVVKI.EPNSI.DOTDMHGDSEVNIMEGEDIG 120
61 SASFEPFSNR

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Search completed: January 9, 2002, 15:02:02 Job time: 189 sec

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OM protein - protein search, using sw model

January 9, 2002, 15:01:18; search time 25.18 Seconds (without alignments) 262.100 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-828-000-3 971 1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΩΙ	CRTC_HUMAN	CRTC_RAT	CRTC_RABIT	CRIC MOUSE	CRTC_DROME	RAL1_ONCVO	CRTC_CAEEL	CRTC_DICDI	CRTC_EUGGR	CRTC_BETVU	CRIC_RICCO	CRTC_PRUAR	CRTC_ORYSA	CRT2_BOVIN	CRTC_NICPL	CRT2_ARATH	CRTC_CHLRE	CRT1_ARATH	CRTC_BERST	CRTC_SCHMA	CRTC_MAIZE	CRT3_ARATH	CRTC_PIG	CALX_MOUSE	CALX_RAT	CALX_CANFA	CALX_HUMAN	CALG_MOUSE	CALG_HUMAN	CALX_SCHPO	CALX_CAEEL	CAX1_ARATH
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Q39917 glycine max Q39994 helianthus Q82709 pisum sativ Q8878 arabidopsis P27825 saccharomyc P28490 canis famil Q9mpo Mesostigma P55201 acinetobact P23224 listeria mo Q01457 lactococcus P45354 haemophilus P18791 streptococc	
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                     "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                       Hochstrassor D.F., Frutiger S., Paquet N., Bairoch A., Ravier F., Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R., Appel R.D., Hughes G.J., "Human liver protein map: a reference database established by microsequencing and gel. comparison.";
                                                                                                                                                                                                                                                         TISSUE-Keratinocytes;
MEDIINE-93162043; PubMed-1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
Vandekerckhove J.;
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PROSTTE; PS00014; ER_TARGET; 1.
PROSTTE; PS00804; CALRETICULIN_1; 1.
PROSTTE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
                                                                                                                                                                                                                                          PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278
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4 X APPROXIMATE REPEATS.
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P-DOMAIN.
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InterPro; IPR000886; ER_target.
                                                                       TISSUE-Liver;
MEDLINE-93162045; PubMed-1286669;
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EMBL; M32294; AAA36582.1; -.
EMBL; AD000092; AAB51176.1; -.
PIR; A37047; A37047.
PIR; A42330; A42330.
PIR; A46423, A46452.
SWISS-2DPAGE; P27797; HUMAN.
AATMUS/GHAIL-2DPAGE; P27797; HUMAN.
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                 Blochem. J. 270:545-548(1990)
                                                     SEQUENCE OF 18-28.
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SEQUENCE OF 18-26.
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"An endoplasmic reticulum protein, calreticulin, is transported into the acrosome of at sperm.",
Exp. Cell Res. 205:101-110(1993).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                               19 EPAVYFKRQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
(CALRETCULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
(CALCIUM-BINDING PROTEIN 3) (CABP3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes C., Patel Y.C.;
Structural homology between the rat calreticulin gene product and
the Onchocerca volvulus antigen Ral-1.";
Nucleic Acids Res. 18:4933-4933(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robinson D.G., Mieskes G.; Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the endoplasmic reticulum."; J. Cell Sci. 107:2705-2717(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90370496; PubMed-2395661;
Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
                                                                                                                                                                                                                                                                                                    Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                  ASP/GLU/LYS-RICH.
BY SIMILARITY.
PREVBMT SECRETION FROM ER.
MISSING (IN REF. 3).
*; BC37C3C0F1054FB2 CRC64;
  1-4.
3 X APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                 100.0%; Score 971; DB 1;
100.0%; Pred. No. 4.8e-80;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-93202172; PubMed-8453984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95181573; PubMed-7876339,
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                                                                                                                                                                                                                           48141
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
255
297
269
283
283
408
417
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417 AA:
244
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273
273
287
351
414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
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P15253;
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DISULFID
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   DOMAIN
REPEAT
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                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                      "Identification of protein disulfide isomerase and calreticulin as autoimmune antigens in LEC strain of rats.";
Biochim. Biophys. Acta 1158-339-344(1993).
-1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
                                       SEQUENCE OF 18-29.
MEDLINE-91054414; PubMed-2241926;
MICHES S., de Mattel M., Lanfredi M., Villa A., Green N.M.,
Maclennan D.H., Meldolesi J., Pozzan T.;
"Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
Biochem. J. 271:473-480(1990).
                                                                                                                                                                                                                                                                                                         MEDLINE-94072621; Pubmed-8251535;
Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
                                                                                                                                                                                       MEDLINE-92360010; Pubmed-1497655;
Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
"Calreticulin is present in the acrosome of spermatids of rat
                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- SUBURIT: MONOMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CALRETICULUM LUMEN.
-1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-1- CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE D-BETA-HYDROXYBUTYRATE DEHYDROGENASE.
Lone Y.C., Bailly A., Latruffe N.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_target.
Pfam; PF00262; Calreticulin; 1.
PROSTE; PS000626; Calreticulin; 1.
PROSTE; PS000014; ER_TRAGET; 1.
PROSTE; PS008003; CALRETICULIN_1; 1.
PROSITE; PS008004; CALRETICULIN_2; 1.
PROSITE; PS008005; CALRETICULIN_2; 1.
PROSITE; PS008005; CALRETICULIN_2; 1.
BROSITE; PS008005; CALRETICULIN_2; 1.
BROSITE; PS008005; CALRETICULIN_2; 1.
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                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 186:668-673(1992).
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P-DOMAIN.
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                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D78308; BAA11345.1; -.
EMBL; X53363; CAA37446.1; -.
EMBL; X13702; CAA31897.1; ALT_SEQ.
EMBL; X79327; CAA55890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LEC; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S04867; S04867.
PIR; S11205; S11205.
PIR; S13045; S13045.
PIR; A49176; A49176.
PIR; S45036; S45036.
PIR; JH0819; JH0819.
                                                                                                                                                             SEQUENCE OF 18-32
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REPEAT
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SEQUENCE FROM N.A.
TISSUE-Slow-twitch skeletal muscle;
MEDLINE-90094320; PubMed-2600080;
Fliegel L., Burns K., Maclennan D.H., Reithmeier R.A.F., Michalak M.;
"Molecular cloning of the high affinity calcium-binding protein
(calreticulin) of skeletal muscle sarcoplasmic reticulum.";
J. Biol. Chem. 264:21522-21528(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91201375; PubMed-2016321;
Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
Vance J.E., Opas M., Michalak M.;
"Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       1 EPAVÝFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                           18 DPAIYFKEQFLDGDAWTNRWVESKHKSDFGKFVLSSGKFYGDQEKDKGLQTSQDARFYAL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91054414; PubMed=2241926; Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M., MacLennan D.H., Meldolesi J., Pozzan T.; "Calreticulin is a candidate for a calsequestrin-like function i Ca2(+)-storage compartments (calciosomes) of liver and brain."; Biochem. J. 271:473-480(1990).
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MEDLINE=91282795; PubMed=2059224;
Fliegel L., Michalak M.;
Fliegel L., Michalak M.;
Fract-twitch and slow-twitch skeletal muscles express the same isoform of calreticulin.";
Biochem. Biophys. Res. Commun. 177:979-984(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                                                                                                                                                                                   Length 416;
                                                                                                                                                                               Score 933, DB 1; Length 41
Pred. No. 1.2e-76;
5; Mismatches 5; Indels
                                                                   ASP/GLU/LYS-RICH.
BY SIMILARITY.
PREVENT SECRETION FROM ER.
2E6713CED31A2970 CRC64;
   X APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AA
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                                                                                                                            MW;
                                                                                                                                                                               Query Match 96.1%;
Best Local Similarity 94.4%;
Matches 170; Conservative
                                                                                                                          47995
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297
269
283
283
407
163
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                                         Calcium-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> T (IN REF. 5).
B6082B689DC763A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-DOMAIN.
4 X APPROXIMATE REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALRETICULIN
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-DOMAIN.
P-DOMAIN.
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InterPro; IPR000886; ER_target.
                               MEDLINE-92002038; PubMed-1911780;
                                                                                                                                                                                                                                                                                                                                                           calreticulin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Endoplasmic reticulum;
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PIR, E33208; E33208.
PIR; F33208; F33208.
PIR; S13046; S13046.
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PIR; C33208; C33208.
PIR; D33208; D33208.
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DOMAIN
DISULFID
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                                             0; Gaps
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                                                                                                                              18 EPVVYFKEQFLDGDGWTERWIESKHKSDFGKFVLSSGKFYGDQEKDKGLQTSQDARFYAL 77
  Length 418;
95.9%; Score 931; DB 1; Length 41
95.6%; Pred. No. 1.9e-76;
iive 1; Mismatches 7; Indels
Query Match
Bost Local Similarity 95.6
Matches 172; Conservative
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121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLÉ 180
              138 GPGTKKVHVIENYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                 Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.; "Covalent structure of bovine brain calreticulin."; Biochem. J. 298.432-442(1994).
-!- FUNCTION: THIS PROFEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..).
PREVENT SECRETION FROM ER (POTENTIAL).
7D4B68DFC689EEF1 CRC64;
                                                                                                                                                                       Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNT: MONOMER.
-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-1- SIMILARITY: BELOMES TO THE CALRETICULIN FAMILY.
InterPro: IPR001580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-DOMAIN.
4 X APPROXIMATE REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO0626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-DOMAIN
                                                                                                                                                                                                                                                                                     MEDLINE-94183174; PubMed-8135753;
                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-0CT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00262; calreticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 171; Conservative
                                                                                             STANDARD;
                                                                                                                                                                                                     Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
256
270
334
120
162
397
400 AA;
                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
292
1174
1174
1193
227
242
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                                                                                           CRT1_BOVIN
P52193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DISULFID
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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REPEAT
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REPEAT
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                                                                   RESULT 4
CRT1_BOVIN
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416 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                      REPEAT
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                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
MEDLINE-93013037; PubMed-1398135;
Mazzarella R.A., Gold P., Cunningham M., Green M.;
"Determination of the sequence of an expressible cDNA clone encoding ERP60/cairegulin by the use of a novel nested set method.";
Gene 120:217-225(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein."; EMBO J. 8:3581-3586(1989).
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRODGS; CALREITCULIN.
PRODOM; PD001866; CALREITCULIN.
PROSTIE; PS00014; ER_TARGET; 1.
PROSTIE; PS00803; CALREITCULIN_1; 1.
PROSTIE; PS00804; CALREITCULIN_2; 1.
PROSTIE; PS00805; CALREITCULIN_Z; 1.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-90059955; Pubmed-2583110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALRETICULIN. N-DOMAIN.
                                                                                                                                                              416
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EMBL, M92988; AAA37569.1; --
PIR, S06763, S06763.
PIR, JC1444; JC1444,
SWISS-2DPAGE; P14211; MOUSE.
MGD; MGT:88252; Calr.
InterPro; IPR001580; Calreticulin.
InterPro; IPR001886; ER_target.
Pfam; PF00262; Calreticulin; 1.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith M.J., Koch G.L.E.;
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fibroblast;
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                                                                                                                                                           CRTC_MOUSE
P14211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                        RESULT 5
CRTC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Hilp P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A button G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.K., Bouve, J., Brokstein P., Brottler P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of a Drosophila melanogaster gene encoding calreticulin homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                          ER.
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
PREVENT SECRETION FROM ER
24C03B00913408D8 CRC64;
                              4 X APPROXIMATE REPEATS
                                                                                                                                                                       X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRTC_DROME STANDARD; PRT; 406 AA. P29411; Q9VHA3; 01-APR-1993 (Rel. 25, Created) 01-OCT-1993 (Rel. 27, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 930; DB 1; I
Pred. No. 2.3e-76;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                               ASP/GLU/LYS-RICH.
C-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE-93208374; PubMed-1296819;
                                                                                                                                                                                                                                                                                                                                                                                   47994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 94.4
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calreticulin homologue.";
DNA Seq. 3:247-250(1992).
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A. Glodek A., Gong F., Gornell J.H., Gul Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jaali M., Kalush F., Karjen G. H., Krayitz S., Kulp D., Lai Z., Liang Y., Lin X., Karmison B.E., Kodira C.D., Krayitz G., Krayitz S., Kulp D., Lai Z., Lang Y., Lin X., Martia B., McInchosh T.C., Mcrayitz J., Mobhrefi A., Morkidov G., Milshina N.V., Mobbary C., Morris J., Mosherfi D., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Mount S.M., Moy M., Murphy B., Murphy L., Scheeler F., Shen H., Nelson K.A., Nixon K., Nusskern D.R., Parlaxaolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Spredling A.C., Stapleton M., Strong R., Sun E., Sheng L., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Weils S.M., Woodage T., Worley W., Zhang G., Zhan G., Zhan M., Zhang G., Zhan G., Zhan K., Zhang K.H., Zhang K.H., Zhang R.N., Walssenbach J., Langson M., Strong R., Shang X., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., The gonome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE~90307981; PubMed~2365822;
McCaullffa D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A human Ro/SS-A autoantigen is the homologue of calreticulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003683; AAF5446.1; -...
PIR, A37158, A37158.

FlyBase; FB900005585, Crc.
InterPro; IPR000886; ER_target.
InterPro; IPR000886; ER_target.
Pfam; PF00262; calreticulin; 1...
Probom; PR00666; Calreticulin; 1...
Probom; PS00014; ER_TARGET; 1...
PROSITE; PS00014; ER_TARGET; 1...
PROSITE; PS00804; CALRETICULIN_1; 1...
PROSITE; PS00804; CALRETICULIN_2; 1...
PROSITE; PS00805; CALRETICULIN_2; 1...
PROSITE; PS00805; CALRETICULIN_2; 1...
PROSITE; PS00805; CALRETICULIN_1; 1...
PROSITE; PS00805; CALRETICULIN_2; 1...
PROSITE; PS00805; CALRETICULIN_1; 1...
PROSITE; PS00805; CALRETICULIN_2; 1...
PROSITE; PS00805; CALRETICULIN_3; PS0080
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V -> L (IN REF. 3).
; 65D72C69D0BEC427 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 91-124 AND 182-220
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406 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capra J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 53-388 FROM N.A.
MEDLINE-88273584; PubMed=2455736;
Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
Isolation and characterization of expression cDNA clones encoding antigens of Onchocerca volvulus infective larvae.";
J. Clin. Invest. 82:262-269(1988).
-: SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioldea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                          Rokeach L.A., Zimmerman P.A., Unnasch T.R.; "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the calreticulin family of proteins, recognized by sera from patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
9537F298A2D31CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Antigen; Signal.

17 POTENTIAL.
388 RAL-1 PROFEIN.
253 4 X APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH (BASIC).
                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
                                                                                                               388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001580; calretlculin.
Pfam; PF00262; calretlculin; 1.
PRINTS; PR00626; CALRETICULIN.
                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 62:3696-3704(1994).
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=94341871; PubMed=7520419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20565; AAA59056.1; -. PIR; A32507; A32507.
                                                                                                               STANDARD;
                                                                                                                                                                                                                            Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257
271
285
353
135
388 AA;
                                                                                                                                                                                                                                                                                                                                                                                            onchocerciasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding;
                                                                                                                                                                                                                                                                           NCBI_TaxID-6282;
                                                                                                               RAL1_ONCVO
P11012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                RAL1_ONCVO
                                                                             RESULT
```

;; 7

Gaps

;

30; Indels

14; Mismatches

Matches 132; Conservative

Query Match Best Local Similarity

72.0%; Score 699; DB 1; Length 406; 74.2%; Pred. No. 1.3e-55;

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STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                             CRTC_DICDI
                                                                       DISULFID
                                                                                           SEQUENCE
                   DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                          RESULT 9
CRTC_DICDI
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                                                                                                      FE-PFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
                                                                                                                 Gaps
                                                                        4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                             123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                         DNA Seq. 2:235-240(1992).
-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                         5,
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-92329978; Pubmed-1627827;
Smith M.J.;
A. C. elegans gene encodes a protein homologous to mammalian calreticulin.";
                     Length 388;
                                         30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0803; CALRETICULIN 1; 1.
PROSITE; PSO0804; CALRETICULIN 2; 1.
PROSITE; PSO0805; CALRETICULIN REPEAT; 3.
Endoplasmic reticulum; Calcium binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-DOMAIN.
4 X APPROXIMATE REPEATS.
1-1.
1-2.
                   68.4%; Score 664; DB 1;
67.4%; Pred. No. 1.7e-52;
iive 26; Mismatches 30;
                                                                                                                                                                                                                                           01-AVG-1992 (Rel. 23, Created)
01-AVG-1992 (Rel. 23, Last sequence update)
01-EB-1994 (Rel. 28, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                       395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALRETICULIN.
N-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S25851; S25851.
InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; Exterrget.
Pfam; PF00252; Calreticulin; 1.
PRINTS; PR00626; CALRETICULIN; 1.
ProDom; PD001866; Calreticulin; 1.
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59589; CAA42159.1; -.
                                         Matches 120; Conservative
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
302
186
186
205
                                                                                                                                                                                                                     CRTC_CAEEL
P27798:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                      64
                                                                                                                                                                                                           CRTC_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                 64 FE-PFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                            4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                                                                                  17 VYFKEEFNDA-SWEKRWVQSKHKDDFGAFKLSAGKFFDVESRDQGIQTSQDAKFYSRAAK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIGH AND
                                                                                                                                                                                                                                               Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAĽ.
CALRETICULIN.
4 x 12 AA APPROXIMATE REPEATS.
1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
1-3.
3 X APPROXIMATE REPEATS.
2-1.
2-3.
ASP/GLU/LYS-RICH.
BY SIMILARITY.
                                                                                                                                                                 PREVENT SECRETION FROM ER. 35CA7D2EC1D56B03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-binding; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CALRETICULIN PRECURSOR.
Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostellida; Dictyostellum.
                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                            Query Match 63.8%; Score 619.5; DB 1
Best Local Similarity 63.5%; Pred. No. 1.7e-48;
Matches 113; Conservative 26; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro: IPR001880; Calreticulin.
Interpro: IPR001886; ER_target.
Interpro: IPR001886; ER_target.
PRIM: PR001626; Calreticulin: 1.
PR018: PR001866; Calreticulin: 1.
PR05ITE; PS00804; CALRETICULIN_2; 1.
PR05ITE; PS00804; CALRETICULIN_2; 1.
PR05ITE; PS00014; ER_TARGET: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA
                                                                                                                                                                                      MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U36937; AAB87719.1; -.
                                                                                                                                                                                      45616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
424
257
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum;
    222
239
254
254
268
282
332
392
392
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DictyDb; DD00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
NAVWAZIO L., Baldan B., Martin W., Mariani P.;
"Evidence for conservation of a calcium homeostat component:
purification characterization and cloning of calreticulin from Euglena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOM AFFIRITY CALCIUM-BINDING SITES (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                      GPGTKKVHVIFNYKGKNVLINKDI-RCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                               4 VYFKEQFLDGDGWTSRWIESK-HKSD--FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                               PREVENT SECRETION FROM ER (POTENTIAL).
BAF273694FB6FC37 CRC64;
                                                                                                                                                                                                                   .
8
                                                                                                                                                                                   55.3%; Score 537; DB 1; Length 424; 57.2%; Pred. No. 4.7e-41;
1-2.
1-3.
1-4.
3 X 11 AA APPROXIMATE REPEATS.
2-1.
                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probon, PD001866, Calreticulin, 1.
PROSTE; PS00014; ER_TARGET; 1.
PROSTIE; PS00803; CALRETICULIN_1; 1.
PROSTIE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_Z; 1.
ROSITE; PS00805; CALRETICULIN_REPEAT; FALSE_NEG.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euglena gracilis.
Eukaryota: Euglenozoa; Euglenida; Euglenales; Euglena.
NCBI_TaxID-3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA
                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALRETICULIN
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InterPro; IPR000886; ER target.
Pfam; PF00262; calreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y09816; CAA70945.1; -.
                                                                                                                                         48350
                                                                                                                                                                                                 Best Local Similarity 57.2*
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALRETICULIN PRECURSOR.
                                                                                                                                         424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001
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                                                                                                                       SITE
SEQUENCE
                                                                                                           DISULFID
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZNY3;
REPEAT
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DOMAIN
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
CRTC_EUGGR
                                                                                                                                                                                                                                                                                                                                                                     121
 STITITIES
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InterPro; IPR001580; Calreticulin.
InterPro; IPR001686; ER_target.
Pram; Pr00262; Calreticulin; IPR001866; Calreticulin; IPR001866; Calreticulin; IPR05186; Calreticulin; IPR05186; Calreticulin; IPR05186; PS00014; ER_TARGET; IPR05186; PS00004; CALRETICULIN_1; IPR0518; PS00804; CALRETICULIN_2; IPR0518; PS00805; CALRETICULIN_2; IPR0518; PS00805; CALRETICULIN_3; IPR0518, IRR0518, IRR0518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 F-EPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGF 122
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 IYYKETF--EPDWETRWTHSTAKSDYGKFKLTSGKFYGDKAKDAGIQTSQDAKFYAISSP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:|| | |||||:| |: ||: ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
      PREVENT SECRETION FROM ER (POTENTIAL). 056B074C16292674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
565FBC34B9F77CA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta vulgaris (Sugar beet).
Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllidae; Caryophyllidae; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                             DB 1; Length 401;
                                                                                                                                                                                                                                                                                                                                                          42; Indels
                                                                                                                                                                                                                                55.1%; Score 535.5; DB 56.7%; Pred. No. 6e-41; tive 30; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
398 401 P
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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416 AA;
                                                                                                                                                                                                                                                                                                   Similarity
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O81919;
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                                                                                                                                                                                                                                                                                                                                                          Matches 101;
                                                            SEQUENCE
                                                                                                                                                                                                                                Query Match
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Gaps

Indels

43;

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Conservative

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Matches
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                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00014; ER_TARGET: I.
PROSITE: PS00004; CALRETCULIN 1; 1.
PROSITE: PS00004; CALRETCULIN 2: 1.
PROSITE: PS000064; CALRETCULIN 2: 1.
PROSITE: PS000064; CALRETCULIN REPEAT; 2.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
SIGNAL 1 20 POTENTIAL.
CHARN 21 415 N-LINKED (GLCNAC. ..) (POTENTIAL).
CARBOHYD 52 52 N-LINKED (GLCNAC. ..) (POTENTIAL).
SITE 412 H5 A3, 47522 MW; DD5F452E76CC7F8C CRC64;
                                                                                                        SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                       Eukaryota; Viridiplantae; Stréptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                              Gaps
                                                                    27 VFFEERF--EDGWEKRWVKSEWKKDESMAGEWNYTSGKWNGD-ANDKGIQTSEDYRFYAI 83
                                                    4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                           121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE-97435975; Pubwed-9290642;
Coughlan S.J., Hastings C., Winfrey R. Jr.;
Cloning and characterization of the calreticulin gene from Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 34:897-911(1997).
-!- FUNCTION: THES PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                              9
    Length 416;
                              45; Indels
  54.7%; Score 531; DB 1; 55.9%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                      415 AA
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendel; 10452; Ricco;1166;10452.
InterPro; IPR001580; Calreticulin.
InterPro; IPR001886; Extraget.
Pfan; PF00262; calreticulin; I.
PRIMTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; I.
                            28;
                                                                                                                                                                                                                                                                                                                                   (Castor bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U74631; AAB71420.1; -. EMBL; U74630; AAB71419.1; -.
                            Matches 100; Conservative
                                                                                                                                                                                                                                                      STANDARD;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-3988;
                                                                                                                                                                                                                                                      CRTC_RICCO
P93508;
                                                                                                                                                                                                                        RESULT 12
CRTC_RICCO
                                                                                                        61
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Length 415;

Score 527; DB 1; Pred. No. 3.6e-40;

54.3%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and nuclectide sequence of a calreticulin from apricot (Prunus armeniaca cv. Bergeron).";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
--- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD001866; Calreticulin; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00804; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
ERGSTE; PS00805; CALRETICULIN_REPRAT; 2.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
SIGNAL
                                                                                                                                                  SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                               22 VFFEERF--EDGWENRWVKSDWKKDENTAGEWNYTSGKWNGD-PNDKGIQTSEDYRFYAI 78
                                                                                                                                                                                                                                    121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
+ 4FSF94CBAAGC6690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-CV. BERGERON; TISSUE-Mesocarp, and Endocarp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALRETICULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mbeguie-A-Mbeguie D., Fils-Lycaon B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eurosids I; Rosales; Rosaceae; Prunus
NCBI_TaxID=36596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF134733; AAD32207.1; -.
InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_target.
Pfam: PF00262; calreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prunus armeniaca (Apricot).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRTC_PRUAR
Q9XF98;
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CRTC_PRUAR
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                                    g
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGTVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                             PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN REPRAT; 1.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
VFFEERF -- EDGWDKRWVTSEWKKDENLAGEWNYTSGKWNGD-PNDKGIQTSEDYRFYAI 82
                                                                                                                    GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALRETICULIN.
N-LINRED (GLCNAC. ..) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL)
3172634F1580FC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 527; DB 1; Length 424; 55.9%; Pred. No. 3.7e-40; 1.ve 31; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                           424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB021259; BAA88900.1; -.
InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER_target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00262; calreticulin; 1.
                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.9%
Matches 100; Conservative
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TuxID-4530;
                                                                                                                                                                                                                                                       CRTC_ORYSA
Q9SLY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
                                  121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. acta 1202:70-76(1993).
-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW APPINITY CALCIUM-BINDING SITES.
-!- SUBUNIT: MONOMER (EY SIMILARITY).
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu N., Fine R.E., Johnson R.J.; "Comparison of cDNAs from bovine brain coding for two isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
PREVENT SECRETION FROM ER.
0257E959F71528BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
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InterPro; IPR001880; Calreticulin.
InterPro; IPR001886; ER_target.
Pfam; PF00262; Calreticulin; I.
PRINTS; PR00626; Calreticulin; I.
PRODOM; PB001866; Calreticulin; I.
PROSITE; PS00801; ER_TARGET; I.
PROSITE; PS00803; CALRETICULIN_1; I.
PROSITE; PS00804; CALRETICULIN_2; I.
PROSITE; PS00805; CALRETICULIN_2; I.
PROSITE; PS00805; CALRETICULIN_2; I.
PROSITE; PS00805; CALRETICULIN_BERAT; 3.
Endophasmic reticulum; Calculum-binding; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALRETICULIN, BRAIN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 X APPROXIMATE REPEATS. 2-1.
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BY SIMILARITY.
                                                                                                                                                                                                                                   421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93385184; PubMed-8373827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
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                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos
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421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calreticulin.
                                                                                                                                                                                                                             CRT2_BOVIN
P42918;
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53.8%; Score 522.5; DB 1; Length 421;

Gaps

45;

1 EPAVYFKEQFLDGDGWTSRWIESKHKSD-------FGKFVLSSGKFYGDEE 44 Best Local Similarity 55.6%; Pred. No. 9.4e-40; Matches 109; Conservative 12; Mismatches 30; Indels 165 YEVKIDNSQVESGSLE 180 186 YEVKIDNSQVESGSLE 201 ò g ò g ò Q ò

Search completed: January 9, 2002, 15:12:14 Job time: 656 sec

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January 9, 2002, 14:58:58; Search time 78.15 Seconds (without alignments) 336.904 Million cell updates/sec
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971
1 EPAVYFKEQFLDGDGWTSRW......PDNTYEVKIDNSQVESGSLE 180
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                   473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
sp_virus:*
sp_vurclebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_fung1:*
sp_human:*
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sp_moretebrate:*
sp_mammal:*
sp_organelle:*
sp_organelle:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		\$ Ouerv				
NO.	Score	Match	Match Length DB	DB	ID	Description
	835	86.0	411	13	091710	Q91710 xenopus lae
7	804	82.8	405	Ŋ	Q26268	Q26268 aplysia cal
Э	797	82.1	343	13	091711	091711 xenopus lae
4	196	82.0	419	13	098984	Q98984 rana ruqosa
S	785	80.8	417	13	Q9PUC1	Oppucl brachydanio
9	759	78.2	410	Ŋ	Q16893	Q16893 amblyomma a
7	731	75.3	421	Ŋ	080680	Q9u6s0 strongyloce
æ	669	72.0	406	Ŋ	090916	Q9u916 drosophila
σ	681.5	70.2	403	S	076961	076961 necator ame
10	680	70.0	387	ហ	097372	097372 dirofilaria
11	673	69.3	375	Ŋ	018478	018478 litomosoide
12	641	0.99	380	11	906060	Q9d9q6 mus musculu
13	539	55.5	412	10	040040	Q40040 hordeum vul
14	539	55.5	415	10	Q40041	Q40041 hordeum vul
15	536	55.2	421	10	043712	Q43712 zea mays (m
16	517	53.2	389	10	040567	040567 nicotiana t
17	514.5	53.0	427	10	Q9FYV2	Q9fyv2 pinus taeda
18	507.5	52.3	396	2	045034	045034 schistosoma
19	477.5	49.2	350	S	026514	Q26514 schistosoma

20 464.5 47.8 240 10 Q9ST29 21 460 47.4 318 13 Q9PTX7 22 446.5 46.2 40.3 5 Q9VDG2 24 446.5 46.0 40.1 5 Q9UDG2 25 40.9 5 42.2 29.1 5 Q9V1V1 26 39.2 40.4 32.1 13 Q9USG0 27 37.3 38.4 32.1 13 Q9USG0 28 34.7 35.7 42.2 10 Q25.02 29 329.5 33.9 32.9 10 Q4751 31 289.5 29.8 582 3 Q9PKC5 32 262 27.0 678 11 Q9DXK5 33 264.5 27.2 559 5 Q9USK5 34 263.5 27.1 581 5 Q9BKH3 35 264.5 27.1 581 5 Q9RK6 36 251 25.8 70 QSXW3 37 248 25.5 582 5 Q9VXF6 38 240 24.7 583 5 Q9VXF6 38 224 55.5 582 5 Q9VYF4 41 231.5 23.8 5 Q9VYP4 42 224 23.1 556 5 Q91YP4 43 221.5 22.8 605 5 Q02393 450 470 471 556 5 Q9VYP7 41 221.5 22.8 605 5 Q91YP4 42 221.5 22.8 605 5 Q9VYP7	Q9st29 solanum mel O9ptx7 lampetra re O9udg2 homo sapien Q9xyf8 trypanosoma Q9u9n9 trypanosoma Q9u5n9 trypanosoma Q9u5n9 trypanosoma Q9u5n9 trypanosoma Q9u5n9 ptatretus O22502 brassiga na Q41799 zea mays (m Q40751 parthenium Q9hfc6 yarrowia li Q9dZx5 mus musculu Q9dXx9 mus musculu Q9dXx6 fritichomo Q9blha haloxophila Q9sxx3 lithospermu Q04702 schistosoma Q9vxf6 drosophila Q9vxf6 drosophila Q9iyp4 drosophila Q9iyg4 drosophila Q9iyal drosophila
464.5 47.8 240 10 460 47.4 318 13 448.5 46.2 46.2 401 5 449.5 46.2 401 5 409.5 42.2 291 5 373 38.4 321 13 329.5 33.9 32.1 13 329.5 33.9 321 10 329.5 29.8 582 3 262 52.0 622 13 264.5 27.1 581 5 263.5 27.1 581 5 263.5 27.1 581 5 263.5 27.1 581 5 263.5 27.2 582 5 238.5 24.6 582 5	0958729 09PTX7 09DD62 09YDD62 09YD02 094592 094560 041799 040751 040751 040751 091560 0916094 091783 091783 091783 091783 091783 091783
464.5 466.5 47.8 48.50 48.60 49.55 409.5	
464.5 460.5 444.8 446.5 409.5 302.5 302.5 302.5 262.2 262.2 262.2 240.2 240.2 240.2 240.2 240.2 240.2 240.2 240.2 240.2 240.2	0 4 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2
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01000000000000000000000000000000000000	464.5 460.5 444.50 446.5 446.5 446.5 409.5 3302.5 200.
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## ALIGNMENTS

RESULT

Query Match 86.0%; Score 835; DB 13; Length 411;
Best Local Similarity 83.9%; Pred. No. 2.7e-71;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps

us-09-828-000-3.rspt

-13

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936369

133

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Pfam; PF00262; calreticulin; 1.
PRINWS; PR00626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN. 1.
PROSITE; PS00803; CALRETICULIN.; 1.
PROSITE; PS00804; CALRETICULIN.; 1.
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BMBL; D78689; BAA14251.; -.
InterPro; IPR000886; ER_target.
InterPro; IPR001580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-96234004; PubMed-8654561;
                                                                                                           MEDLINE-93074997; PubMed=1445218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frog, Rana rugosa.";
FEBS Lett. 387:27-32(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALRETICULIN.
                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto S.;
                                                                                                                                                                             system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q98984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93098937; Pubmed-1463604;
MEDLINE-93098937; Pubmed-1463604;
Mennedy T.E., Kuhl D., Barzilal A., Sweatt J.D., Kandel E.R.;
Kannedy T.E., Kuhl D., Barzilal A., Sweatt J.D., Kandel E.R.;
Kannedy T.E., Kuhl D., Barzilal A., Sweatt J.D., Kandel E.R.;
T.Long term sensitization training in Aplysia leads to an increase in the calreticulin, a major presynaptic calcium-binding protein.";
Rull, S$1239; AABA2691; -.

Rull, S$1239; AABA2691; -.

Rull, S$1239; AABA26691; -.

Rull, S$1239; ABBA2691; ABBA269184091099; CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                      SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
                                                                                                             121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                      GPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLIYTLIVRPDNTYEVKIDNSKVESGSLE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 DPTVYFKEEF--GDDWAERWVESKHKSDLGKFVLTAGKFYGDAEKDKGIQTSQDARFYGL 73
EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-JAN-1998 (TrEMBLrol. 05, Last sequence update)
01-JUN-2001 (TrEMBLrol. 17, Last annotation update)
CALRETICULIN (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 82.8%; Score 804; DB 5; Local Similarity 79.4%; Pred. No. 2.3e-68; Nes 143; Conservative 18; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 AA
                                                                                                                                                                                                                                                                                                                                 405 AA
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Best Local Similarity 79.44
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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NCBI_TaxID-6500;
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61 QTLVIQESVKHEQNIDCGGGGYVKLFPADLEQTEMHGESEYNIMFGFDICGPPTKKVHVIF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 QTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGPGTKKVHVIF 131
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 DGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSASFEPFSNKG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto S., Nakamura M.; "Calnexin: its molecular cloning and expression in the liver of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana rugosa (Frog).
Rakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8410;
Treves S., Zorzato F., Pozzan T.; "Identification of calreticulin isoforms in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                    82.1%; Score 797; DB 13; Length 343;
85.2%; Pred. No. 8.7e-68;
tive 12; Mismatches 13; Indels
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J. Exp. 2001. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 343
343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Amblyomma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-SALIVARY GLANDS;
Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32CCB8750A17DC54 CRC64;
                                                         Last sequence update)
Last annotation update)
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Last annotation update)
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     410 AA
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PRODOM; PO01866; Calreticulin; 1.
PROSITE; PSO0803; CALRETICULIN.1, 1.
PROSITE; PSO0805; CALRETICULIN.1, 1.
PROSITE; PSO0014; ER_TARGET; UNKNOWN.1.
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     PRT;
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InterPro; IPR000886; ER_target.
InterPro; IPR001580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00262; calreticulin; 1.
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17,
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                                                                                                                                                                                                                                 SEQUENCE OF 49-410 FROM N.A.
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.7%
Matches 138; Conservative
                                       01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-SALIVARY GLANDS;
Jaworski D.C.;
                                                                                                                                                                                                                                                     IISSUE=SALIVARY GLANDS;
                                                                                                                                     Amblyomma americanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=6943;
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                                                                                                                                                                                                                                                                                           Needham G.R.;
                                                                                               CALRETICULIN.
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                         016893;
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Q9U6S0
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                                                                                                                                                                                                                                                                                                                                              139 GPPTKKVHVIFNYKGKNLQINKDIRSKADVYSHLYTLIVRPDNTYEVKIDNSKVESGNLE 198
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                                                                                                                                                                                                                                                   SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
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                                                                                                                                                                         1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60
                                                                                                                                                                                             4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 VYFKEQFLDGDGWKSRWVESKHKSDYGQWKLTSGKFYGDPELDKGLQTSGDARFYALSSR 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).

Brustyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.; "Genes Dependent on Zebrafish cyclops Function Identified by AFLP
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                                                                                               Length 419;
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InterPro; IPR000886; ER_target.

InterPro; IPR001880; Calreticulin.

Pram; PF00262; calreticulin; 1.

PR00565; Calreticulin; 1.

PR0057E; PS00804; CALRETICULIN; 1.

PROSITE; PS00804; CALRETICULIN_1; 1.

PROSITE; PS00804; CALRETICULIN_2; 1.

PROSITE; PS00805; CALRETICULIN_2; 1.

PROSITE; PS008014; ER_TARGET; UNKNOWN_1.

SEQUENCE 417 AA; 48723 MW; 2000C5B400469986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                   16; Indels
PS00805; CALRETICULIN REPEAT; 3.
PS00014; ER_TARGET; UNKNOWN_1.
419 AA; 48658 MW; 2C857036769673BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                         82.0%; Score 796; DB 13;
80.6%; Pred. No. 1.4e-67;
iive 19; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.8%; Score 785; DB 13; 79.7%; Pred. No. 1.5e-66; ive 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differential Gene Expression Screen."; Genesis 0:0-0(1999).
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Best Local Similarity 79.7%
Matches 141; Conservative
                                                                                                             Best Local Similarity 80.6
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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 PROSITE;
PROSITE;
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Length 410

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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         403 AA
    Matches 132; Conservative 14; Mismatches
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PRINES; PR00626; CALRETICULIN; 1.
PROSITE; PS001866; CALRETICULIN; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPRY; PROSITE; PS008014; ER_TARGET; UNKNOWN_1.
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46833 MW;
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Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Necator americanus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Allergen.
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097372;
01-MAY-1999 (
01-MAY-1999 (
01-JUN-2001 (
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076961;
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097372
ID 097372
AC 097372;
DT 01-MAY-
DT 01-JUNY-
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076961
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CRC OR CG4249.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota, Meoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
                Susan J.M., Just M.L., Lennarz W.J.;
"Cloning and Characterization of AlphaP Integrin and Calreticulin in Embryos of the Sea Urchin.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF177915; AAD55725.1; -.
InterPro; IPR000886; ER_target.
InterPro; IPR001886; ER_target.
PRINTS; PR00466; Calreticulin.
PRINTS; PR00466; Calreticulin, 1.
PRINTS; PR00466; Calreticulin; 1.
PROSTIE; PS00804; CALRETICULIN.
PROSTIE; PS00804; CALRETICULIN. 2; 1.
PROSTIE; PS00804; CALRETICULIN. REPEAR; 3.
PROSTIE; PS00804; ER_TARGET; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SFEPFSNKGOTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VYFEDQFADA-SWESRWVESVHKGSDAGKFKWSAGKFYGDAEQDKGIQTSQDAKFYGLSA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VYFKEQFLDGDGWTSRWIESKHK-SDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN—OREGON-K;
Dodo K., Sakoyama Y., Gamo S.;
Drogophila melanogastor calreticulin for mRNA.";
Lubmitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AB000/18; BAR85379.1;
Ribase; Fagn0005585; Crc.
R niterPro; IPR001868; ER.target.
R niterPro; IPR001868; ER.target.
Probom; PR00262; calreticulin, I.
PROSITE; PR00865; Calreticulin, I.
PROSITE; PR00865; Calreticulin, I.
PROSITE; PR00865; Calreticulin, I.
PROSITE; PS00804; CALRETICULIN.2; I.
PROSITE; PS00804; CALRETICULIN.2; I.
PROSITE; PS00804; CALRETICULIN.2; I.
PROSITE; PS00804; CALRETICULIN.2; I.
PROSITE; PS00804; CALRETICULIN.REPEAT; 3.
DR PROSITE; PS00804; CALRETICULIN.REPEAT; 3.
DR PROSITE; PS00804; CALRETICULIN.REPEAT; 3.
DR PROSITE; PS00804; CALRETICULIN.REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
                                                                                                                                                                                                                                                                                            1 19 POTENTIAL.
20 421 CALRETICULIN.
421 AA; 48822 MW; 172C664F59F41F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.3%; Score 731; DB 5; Best Local Similarity 74.7%; Pred. No. 2.1e-61; Matches 133; Conservative 19; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 699; DB 5;
Pred. No. 2.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%;
74.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9U916 Q9U916;

Query Match Best Local

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SIGNAL Signal CHAIN

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                                                                                                                          63 SFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
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                            21 VYLKENF-DNENWEDTWIYSKHPGKEFGKFVLTPGTFYNDAEADKGIQTSQDARFYAASR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                          123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Bunostominae; Necator.
NCBI_TaxID=51031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood Berry C., Fullkrug R., Beck E.;
"Calreticulin is a hookworm allergen.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJOG6790; CAA67254.1;
InterPro; IPRO01580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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21F38B0515487B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALRETICULIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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68.5%; Pred. No. 9.8e-57;
tive 30; Mismatches 23
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2; Gaps

Indels

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
B., Haseliashi R., Kawaji H., Kohtsuki S.,
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                                                                                                                                                 64 FEP-FSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDICGP 122
                                                                   19 VYFKEEFLD-DEWENRWIKSKHKDDFGKWEISHGKFYGDAVKDKGLKTTQDAKFYSIGAK 77
                                            4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS 63
                                                                                                                                                                                                           123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                   4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSSGKFYGDEEKDKGLQTSQDARFYALSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VYFQEEFLDGERWRNRWVQSTNDSQFGHFRVSSGKFYGHKEKDKGLQTTQNSRFYAISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00803; CALRETICULIN_1; 1.
380 AA; 44198 MW; BI3BC4ADBI1B0442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.0%; Score 641; DB 11; Best Local Similarity 65.0%; Pred. No. 6.4e-53; Matches 115; Conservative 30; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                              380 AA
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001580; Calreticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001866; Calreticulin; 1
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                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 17, 00031L01RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK006582; BAB24660.1;
  Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1700031L01RIK.
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SEQUENCE
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090906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 GTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metažoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Litomosoides.
                                            Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-99094497; PubMed-9879888;
Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.
"Molecular characterization of a calcium-binding protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 680; DB 5; Length 387;
Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MacLennan K., Hoffman W.H., Taylor D.W.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, *A1001621; CAA004877.1; -..
InterPro: IRF001580; Calrettculin.
Pfo0262; calreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALRETICULIN.
E7741BF6AAFA5885 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43842 MW; 03F7642FBFF7A5B8 CRC64;
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Last annotation update)
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Pred. No. 5.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score vv.,
68.5%; Pred. No. 1.3e.
+ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 AA
                                                                                                                                                                                                                          MOI. Blochem. Parasitol. 97:69-79(1998).
EMBL; AF052978; AAD03405.1; -.
Interpro; IPR001580; calreticulin.
Pr0125; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN.
PROSITE; PS00803; CALRETICULIN.; 1.
PROSITE; PS00804; CALRETICULIN.; 1.
PROSITE; PS00805; CALRETICULIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN. 1.
PROSITE; PS00803; CALRETICULIN. 1; 1.
PROSITE; PS00804; CALRETICULIN. 2; 1.
PROSITE; PS00805; CALRETICULIN.REPEAT; 3.
NON_TER 375 375
SEQUENCE 375 AA; 43842 MW; 03F7642FBFI
                                                                                                                                                                                                           filarial parasite Dirofilaria immitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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68.5%;
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                                     Eukaryota, Metazoa, Nemato
Onchocercidae, Dirofilaria
NCBI_TaxID-6287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.59
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Litomosoides sigmodontis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
387
  CALRETICULIN PRECURSOR
                        Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Signal. SIGNAL

018478

RESULT 11 018478

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Gaps

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Indels

Length 380;

63

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.

C STRAIN-WOREX; TISSUE-OVARY;

RX MEDLINE-94339696; PubMed-7914763;

RA Chen F., Hayes P.M., Mulroony D., Pan A.;

RA Chen F., Hayes P.M., Mulroony D., Pan A.;

RA Chen F., Hayes P.M., Mulroony D., Pan A.;

RA Chen F., Hayes P.M., Mulroony D., Pan A.;

RY Calreticula in barley.";

RL Plant Cell 6:835-843(1994).

RMBL, Lary 348; AAA32948; B.1.

DR RMBL, Lary 348; AAA32948; B.1.

DR Mendel; 8546; Horvu; 1166;886.

InterPro; IPR000886; ER, target.

InterPro; IPR001580; Calreticulin.

InterPro; Alreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordoum vulgure (Barley).
Rukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spormatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Tritticeae; Hordeum.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                          124 TKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
                                                        141 IKKVHVILYFKNQYHENKKPIRCKVDGFTHLYTLILRPDLSYEVKVDGQSIESGSIE 197
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AA; 47037 MW; 37F6C95D6AA78AB0 CRC64;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00162; calreticulfn; 1.
PRINTS; PR0026; CALRETICULIN, 1.
PROSITE; PS001866; CALRETICULIN, 1.
PROSITE; PS00803; CALRETICULIN_2; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN, 2; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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                                                                                                                                                                                                        PRT;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
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                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      CALRETICULIN (FRAGMENT).
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NON_TER
SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae, Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120
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                                                                                    STRAIN-WOREX; TISSUE-OVARY;

BEDIINE-4339666; pubmed-7914763;
Chen F., Hayes P.M., Mulroony D., Pan A.;

Identification and characterization of cDNA clones encoding plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

DISDLINE-96309381; PubMed-8704156;
Dresselhaus T., Hagel C., Loerz H., Kranz E.;
Isolation of a full-length cDNA encoding calreticulin from a PCR "Isolation of a full-length cDNA encoding calreticulin from a PCR library of in vitro zygotes of maize.";
Plant Mol. Biol. 31.23-34(1996).

EMBL; 246772; CAA86728.1;
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J. Exp. Bot. 46:1603-1613(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2897914812FBE33E CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CALCIUM-BINDING PROTREIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.5%; Score 539; DB 10; 56.4%; Pred. No. 3.4e-43; ive 31; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                          Pfam; PF00262; calreticulin; 1.
PRIMES; PR005626; CALRETICULIN; 1.
PROSITE; PS001866; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPRY; PROSITE; PS0014; ER_TARGET; UNKNOWN_1.
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                                                                                                                                                                     calreticulin in barley.";
Plant Cell 6:835-843(1994).
EMBL, L27349; ARA32940.1; -.
mandel, 8547; Horvu;1166;8547.
InterPro; IPR001886; ER_target.
InterPro; IPR001580; Calreticulin.
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415 AA; 47359 MW;
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Best Local Similarity 56.4%
Matches 101; Conservative
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Triticeae; Hordeum.
NCBI_TaxID=4513;
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                                                                SEQUENCE FROM N.A.
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SIĞNAL 1 25 POTENTIAL.
CHAIN 26 421 CALRETICULIN.
SEQUENCE 421 AA; 48012 MW; 5AAE02B77ED3126D CRC64;
EMBL; X89813; CAA61939.1; -...
Mendel; 11228; Zeama;1166;11228.
InterPro; IPR000886; ER_target.
InterPro; IPR001886; Calreticulin.
Pfam; PF00262; Calreticulin.
PROSTE; PR00626; CALRETICULIN.
PROSTIE; PS00803; CALRETICULIN.
PROSTIE; PS00804; CALRETICULIN.
PROSTIE; PS00804; CALRETICULIN.2; 1.
PROSTIE; PS00804; CALRETICULIN.2; 1.
PROSTIE; PS00804; CALRETICULIN.2; 1.
PROSTIE; PS00804; CALRETICULIN. SEPEAT; 2.
PROSTIE; PS00014; ER_TARGET; UNKNOWN.1.
SIGNAL.
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э; 61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDMHGDSEYNIMFGPDIC 120 121 GPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179 6; Gaps 4 VYFKEQFLDGDGWTSRWIESKHKSD---FGKFVLSSGKFYGDEEKDKGLQTSQDARFYAL 60 144 GYSTKKVHTILTKDGKNHLIKKDVPCETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202 Query Match 55.2%; Score 536; DB 10; Length 421; Best Local Similarity 56.4%; Pred. No. 6.7e-43; Matches 101; Conservative 31; Mismatches 41; Indels g ò g ò

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